```
OM of: US-09-722-377-1 to: EST:*   out_format : pfs

Date: Jul 23, 2002  3:02 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlh
 -Q=/cgn2_1/USPTO_spool/US09722377/runat_19072002_111534_29783/app_query.fasta_1.597
 -DB=EST -QFMT=fastap -SUFFIX=oli.rst -GAPOP=4.500 -GAPEXT=0.050
 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000 -QGAPOP=4.500
 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000 -FGAPOP=6.000
 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000 -DELOP=6.000
 -DELEXT=7.000 -START=1 -MATRIX=oligo -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=300 -ALIGN=15
 -MODE=LOCAL -OUTFMT=pfs -NORM=ext -HEAPSIZE=500 -MINLEN=0
 -MAXLEN=2000000000 -USER=US09722377_@CGN1_1_2896 -NCPU=6
 -ICPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY
 -WAIT -THREADS=1

Search information block:
Query: US-09-722-377-1
Query length: 533
Database: EST:*
Database sequences: 13736207
Database length: -1841457050
Search time (sec): 1685.370000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000


score_list:
Sequence           Strd Orig    ZScore    EScore Len  ! Documentation  ..
```

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 12:19:36 ; Search time 54.54 Seconds
(without alignments)
7214.978 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcggacaaaaaaggggt.....tttccttcagccagggatga 1602

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 383533 seqs, 122816752 residues

Word size : 300

Total number of hits satisfying chosen parameters: 0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description

No matches found

Search completed: July 23, 2002, 13:31:29
Job time: 4313 sec

OM of: US-09-722-377-1 to: Issued_Patents_NA:* out_format : pfs

Date: Jul 23, 2002 3:37 PM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2_1/USPTO_spool/US09722377/runat_19072002_111535_29853/app_query.fasta_1.597
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=oli.rni -GAPOP=4.500
-GAPEXT=0.050 -MINMATCH=0.100 -LOOPCL=0.000 -LOOPEXT=0.000
-QGAPOP=4.500 -QGAPEXT=0.050 -XGAPOP=60.000 -XGAPEXT=60.000
-FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
-DELOP=6.000 -DELEXT=7.000 -START=1 -MATRIX=oligo
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=quality
-THR_MIN=300 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs -NORM=ext
-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09722377_@CGN1_1_52 -NCPU=6 -ICPU=3 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLPXY -WAIT -THREADS=1

Search information block:
Query: US-09-722-377-1
Query length: 533
Database: Issued_Patents_NA:*
Database sequences: 383533
Database length: 122816752
Search time (sec): 50.610000

WARN: XGAPOP and YGAPOP must be equal. Assuming YGAPOP=XGAPOP=60.000
WARN: XGAPEXT and YGAPEXT must be equal. Assuming YGAPEXT=XGAPEXT=60.000

score_list:
Sequence Strd Orig ZScore EScore Len ! Documentation ..

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:27:21 ; Search time 1672.7 Seconds
(without alignments)
12926.479 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcggacaaaaaaggggt.....tttccttcagccagggatga 1602

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 300

Total number of hits satisfying chosen parameters: 5

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	650	40.6	700	10	BE519781	BE519781 HV_CEb002
2	570	35.6	605	9	AV835197	AV835197 AV835197
c 3	479	29.9	669	9	AV945501	AV945501 AV945501
4	451	28.2	798	10	BE558835	BE558835 HV_CEb002
c 5	356	22.2	402	9	AV945620	AV945620 AV945620

ALIGNMENTS

RESULT 1
BE519781
LOCUS BE519781 700 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEb0021D05f Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone HV_CEb0021D05f, mRNA sequence.
ACCESSION BE519781
VERSION BE519781.2 GI:13266203
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 700)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi ,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library
JOURNAL Unpublished (2001)
COMMENT On Aug 8, 2000 this sequence version replaced gi:9743969.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 586
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
High quality sequence stop: 664.
FEATURES Location/Qualifiers
source 1. .700
/organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEb0021D05f"
/clone_lib="Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; C.I. 16151 (Mla6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5874 (AvrMla6) of Blumeria graminis f. sp. hordei, and leaves were harvested 20 and 24 hr post-inoculation and snap frozen; uninoculated leaves were harvested 20 hr post-inoculation (Wei, Wise). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all three RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Close). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum , Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT 149 a 210 c 191 g 150 t
ORIGIN

Query Match 40.6%; Score 650; DB 10; Length 700;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 650; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    280 gtcatgtggccctgcaagcgcggcaccgagggccgcaagcccagcaagtacgttgactac 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTCATGTGGCCCTGCAAGCGCGGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTAC 60

Qy    340 tgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgtcttc 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCCGGAGGGCAAGGTGGCGCTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTC 120

Qy    400 atcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaagccgt 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGT 180

Qy    460 ctcaaaatgagaacatggaagaaatgggagacagagaccacctccttggaataccagttc 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCACCTCCTTGGAATACCAGTTC 240

Qy    520 gcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcgccacctg 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAAATGATCCTGCACGGTTCCGGTTCACGCACCAGACGTCGTTCGTGAAGCGCCACCTG 300

Qy    580 ggcctctccagcacccctggcatcagatgggtggtggcctttcttcaggcagttcttcagg 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCCTCTCCAGCACCCCTGGCATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGG 360

Qy    640 tcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcg 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCAGTCACCAAGGTGGACTACCTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTCG 420

Qy    700 caaaacagcaagttcgacttccacaagtacatcaagaggtcgatggaggacgacttcaag 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAAAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAAG 480

Qy    760 gtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgac 819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTCGTCGTCGGCATCAGCCTCCCGCTGTGGGGTGTGGCGATCCTCACCCTCTTCCTTGAC 540

Qy    820 atcaatggggttggcacgctcatctggatttctttcatccctctcgtgatcctcttgtgt 879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCAATGGGGTTGGCACGCTCATCTGGATTTCTTTCATCCCTCTCGTGATCCTCTTGTGT 600

Qy    880 gttggaaccaagctggagatgatcatcatggagatggccctggagatcca 929
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 GTTGGAACCAAGCTGGAGATGATCATCATGGAGATGGCCCTGGAGATCCA 650
```

RESULT 2
AV835197
LOCUS AV835197 605 bp mRNA linear EST 22-JUN-2001
DEFINITION AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah26o13, mRNA sequence.
ACCESSION AV835197
VERSION AV835197.1 GI:14527286
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 605)
AUTHORS Sato,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2001)
COMMENT Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct submission;
database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES Location/Qualifiers
source 1. .605
/organism="Hordeum vulgare subsp. spontaneum"
/cultivar="H602"
/db_xref="taxon:77009"
/clone="bah26o13"
/clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 131 a 188 c 163 g 122 t 1 others
ORIGIN

Query Match 35.6%; Score 570; DB 9; Length 605;
Best Local Similarity 100.0%; Pred. No. 9.4e-276;
Matches 570; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy    236 accccatcatcgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgca 295
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     36 ACCCCATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCA 95

Qy    296 agcgcggcaccgagggccgcaagcccagcaagtacgttgactactgcccggagggcaagg 355
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     96 AGCGCGGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGG 155

Qy    356 tggcgctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcgg 415
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    156 TGGCGCTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGG 215

Qy    416 tcttccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacat 475
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    216 TCTTCCATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACAT 275

Qy    476 ggaagaaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcac 535
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    276 GGAAGAAATGGGAGACAGAGACCACCTCCTTGGAATACCAGTTCGCAAATGATCCTGCAC 335

Qy    536 ggttccggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcaccc 595
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    336 GGTTCCGGTTCACGCACCAGACGTCGTTCGTGAAGCGCCACCTGGGCCTCTCCAGCACCC 395

Qy    596 ctggcatcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtgg 655
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    396 CTGGCATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGGTCAGTCACCAAGGTGG 455

Qy    656 actacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcg 715
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    456 ACTACCTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTCGCAAAACAGCAAGTTCG 515

Qy    716 acttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatca 775
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    516 ACTTCCACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAAGGTCGTCGTCGGCATCA 575

Qy    776 gcctcccgctgtggggtgtggcgatcctca 805
          |||||||||||||||||||||||||||||
Db    576 GCCTCCCGCTGTGGGGTGTGGCGATCCTCA 605
```

RESULT 3
AV945501/c
LOCUS AV945501 669 bp mRNA linear EST 18-JAN-2002
DEFINITION AV945501 K. Sato unpublished cDNA library, strain H602 adult, heading stage top three leaves Hordeum vulgare subsp. spontaneum cDNA clone bah26o13 3', mRNA sequence.
ACCESSION AV945501
VERSION AV945501.1 GI:18241298
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.

```
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah26o13"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT      131 a    182 c    192 g    163 t      1 others
ORIGIN


  Query Match             29.9%;  Score 479;  DB 9;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 6.7e-230;
  Matches  529;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy   1015 ttcttcatacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggaca 1074
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TTCTTCATACACCTGACGTTGTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGTGGACA 610

Qy   1075 gtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaag 1134
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 GTGGCCACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAG 550

Qy   1135 gtggtggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcg 1194
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 GTGGTCGTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCG 490

Qy   1195 ctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaag 1254
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    489 CTCGTCACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAG 430

Qy   1255 gcgctcaccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatg 1314
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 GCGCTCACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATG 370

Qy   1315 ctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagc 1374
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 CTGATGGCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGC 310

Qy   1375 cggggctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccag 1434
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 CGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAG 250

Qy   1435 agcgcgcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtg 1494
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 AGCGCGCCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTG 190

Qy   1495 gcgcacccggtgcacagactaaatcctaacgacaggaggaggtccgcctc 1544
           ||||||||||||||||||||||||||||||||||||||||||||||||
Db    189 GCGCACCCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTC 140


RESULT   4
BE558835
LOCUS       BE558835                798 bp    mRNA    linear   EST 23-OCT-2001
DEFINITION  HV_CEb0020I08f Hordeum vulgare seedling green leaf EST library
            HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
            HV_CEb0020I08f, mRNA sequence.
ACCESSION   BE558835
VERSION     BE558835.3  GI:16336267
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 798)
  AUTHORS   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D.,
            Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi
            ,D.W., Fenton,R.D., Oates,R. and Main,D.
  TITLE     Development of a genetically and physically anchored EST resource
            for barley genomics: Blumeria infected incompatible (Mla6) seedling
            leaf cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     On Aug 14, 2000 this sequence version replaced gi:13266126.
            Contact: Wing RA
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 458
            Seq primer: AATTAACCCTCACTAAAGGG
            High quality sequence stop: 561.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Hordeum vulgare"
                     /cultivar="CI16151 (Mla6)"
                     /db_xref="taxon:4513"
                     /clone="HV_CEb0020I08f"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0005 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16151 (Mla6) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate 5874 (AvrMla6
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids (Choi, Close). Phagemids were plated and picked
                     at the Clemson University Genomics Institute (CUGI) (Begum
                     , Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      153 a    244 c    241 g    158 t      2 others
ORIGIN


  Query Match             28.2%;  Score 451;  DB 10;  Length 798;
  Best Local Similarity   99.8%;  Pred. No. 8.9e-216;
  Matches  501;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy      1 atgtcggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtg 60
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    197 ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG 256

Qy     61 gcggtggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaag 120
          ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    257 GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAGCACGGCCTCCACAAG 316

Qy    121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    317 CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG 376

Qy    181 aaggcggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggacccc 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    377 AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC 436

Qy    241 atcatcgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgc 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    437 ATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC 496

Qy    301 ggcaccgagggccgcaagcccagcaagtacgttgactactgcccggagggcaaggtggcg 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    497 GGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG 556

Qy    361 ctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttc 420
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    557 CTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGGTCTTC 616

Qy    421 catgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaag 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 CATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAAG 676

Qy    481 aaatgggagacagagaccacct 502
          |||||||||||||||||||||
Db    677 AAATGGGAGACAGAGACCACCT 698


RESULT   5
AV945620/c
LOCUS       AV945620                402 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV945620 K. Sato unpublished cDNA library, strain H602 adult,
            heading stage top three leaves Hordeum vulgare subsp. spontaneum
            cDNA clone bah27g01 3', mRNA sequence.
ACCESSION   AV945620
VERSION     AV945620.1  GI:18241417
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .402
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah27g01"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT       60 a    116 c    127 g     96 t      3 others
ORIGIN
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  Query Match             22.2%;  Score 356;  DB 9;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-168;
  Matches  356;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1189 tacgcgctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacg 1248
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TACGCGCTCGTCACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACG 302

Qy   1249 tccaaggcgctcaccaactggcggaacacggccaaggagaagaagaaagtccgagacacg 1308
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCCAAGGCGCTCACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACG 242

Qy   1309 gacatgctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatg 1368
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GACATGCTGATGGCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATG 182

Qy   1369 ccgagccggggctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgac 1428
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCGAGCCGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGAC 122

Qy   1429 ccccagagcgcgcccacctcgccaaggacccagcaggaggctagggacatgtacccggtt 1488
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CCCCAGAGCGCGCCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTT 62

Qy   1489 gtggtggcgcacccggtgcacagactaaatcctaacgacaggaggaggtccgcctc 1544
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 GTGGTGGCGCACCCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTC 6


Search completed: July 23, 2002, 12:50:50
Job time: 5009 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 23, 2002, 14:23:25 ; Search time 43.76 Seconds
(without alignments)
1170.375 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSSALEADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2788	100.0	533	2	T04481	Mlo protein - barl
2	1941	69.6	544	2	T05952	Mlo-h1 protein - b
3	1792	64.3	537	2	T03797	probable mlo prote
4	1253.5	45.0	573	2	B86247	hypothetical prote
5	1234.5	44.3	583	2	H96640	hypothetical prote
6	1220.5	43.8	570	2	T02582	H. vulgare Mlo pro
7	1101.5	39.5	501	2	B84748	similar to Mlo pro
8	1088	39.0	574	2	F84552	similar to Mlo pro
9	1061	38.1	580	2	B84552	similar to Mlo pro
10	1049	37.6	443	2	E96495	hypothetical prote
11	932.5	33.4	526	2	T01089	hypothetical prote
12	927	33.2	496	2	T00691	H. vulgare Mlo pro
13	853.5	30.6	429	2	T09888	hypothetical prote
14	790.5	28.4	485	2	T47469	hypothetical prote
15	631	22.6	507	2	H86393	protein T24P13.8 [
16	499.5	17.9	447	2	A86244	Barley Mlo protein
17	114	4.1	628	2	AG1469	transporter homolo
18	105.5	3.8	574	2	D91159	probable transport
19	105.5	3.8	574	2	B86005	probable transport
20	105	3.8	628	2	AF1108	transporter homolo
21	103.5	3.7	770	2	G90506	conserved hypothet
22	102.5	3.7	574	2	E65135	hypothetical 64.6K
23	98.5	3.5	453	2	B95135	MATE efflux family
24	97.5	3.5	596	2	T19740	hypothetical prote
25	97	3.5	401	2	E81436	transmembrane tran
26	95.5	3.4	443	2	F71929	heat shock protein
27	95.5	3.4	506	2	A33416	nuclear factor I -
28	95	3.4	335	2	T32209	hypothetical prote
29	95	3.4	453	2	D98003	conserved hypothet
30	95	3.4	3071	2	T50345	vacuolar protein s
31	94.5	3.4	303	2	E88241	protein T22C8.1 [i
32	94.5	3.4	303	2	T25114	hypothetical prote
33	94.5	3.4	338	2	E72264	conserved hypothet
34	94	3.4	395	2	S73732	MG306 homolog A05_
35	94	3.4	599	2	G90476	probable Na+/H+ an
36	93.5	3.4	369	2	I64234	competence locus E
37	93.5	3.4	443	1	D64584	heat shock protein
38	93.5	3.4	554	2	T43211	cytoplasmic signal
39	93.5	3.4	666	2	T43171	cytoplasmic signal
40	93.5	3.4	672	2	T24507	hypothetical prote
41	93.5	3.4	951	2	AC3628	nitrite extrusion
42	92.5	3.3	167	2	C81358	probable integral
43	92.5	3.3	262	1	OTFF3Y	cytochrome-c oxida
44	92.5	3.3	262	2	T09805	cytochrome-c oxida
45	92.5	3.3	512	2	F71839	NADH dehydrogenase

ALIGNMENTS

RESULT 1
T04481
Mlo protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C;Accession: T04481
R;Panstruga, R.; Buschges, R.; Piffanelli, P.; Schulze-lefet, P.
Nucleic Acids Res. 26, 1056-1062, 1998
A;Title: A contiguous 60kb genomic stretch from barley reveals molecular evidence for
A;Reference number: Z15372; MUID:98128007
A;Accession: T04481
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-533 <PAN>
A;Cross-references: EMBL:Y14573; NID:g2894376; PIDN:CAA74909.1; PID:g2894377
A;Experimental source: cv. Ingrid
C;Genetics:
A;Gene: Mlo
A;Map position: 4
A;Introns: 43/3; 116/3; 155/3; 176/1; 204/3; 229/3; 259/2; 276/1; 289/3; 359/3; 402/3
C;Superfamily: barley pathogen resistance protein Mlo

Query Match 100.0%; Score 2788; DB 2; Length 533;
Best Local Similarity 100.0%; Pred. No. 5.9e-232;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120

Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420

Qy     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480

Qy     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533


RESULT   2
T05952
Mlo-h1 protein - barley
C;Species: Hordeum vulgare (barley)
C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C;Accession: T05952
R;Panstruga, R.
submitted to the EMBL Data Library, May 1997
A;Reference number: Z15093
A;Accession: T05952
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-544 <PAN>
A;Cross-references: EMBL:Z95496; PIDN:CAB08860.1
A;Experimental source: cv. Igri
C;Genetics:
A;Gene: Mlo-h1
A;Map position: 4H
A;Introns: 41/3; 139/3; 178/3; 199/1; 282/2; 299/1; 312/3; 382/3
C;Superfamily: barley pathogen resistance protein Mlo

  Query Match             69.6%;  Score 1941;  DB 2;  Length 544;
  Best Local Similarity   69.5%;  Pred. No. 5.3e-159;
  Matches  381;  Conservative   51;  Mismatches   76;  Indels   40;  Gaps    6;

Qy      10 RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGF 69
           ||| :||:|||||| | |:|||| ||| |||||||    |||| ||||||||||||||||
Db       8 RELSDTPTWAVAVVCAVMILVSVAMEHALHKLGHWFHKWRKKALGEALEKMKAELMLVGF 67

Qy      70 ISLLLIVTQDPIIAKICISEDAADVMWPCK--------RGTEGRKPSKY---------- 110
           |||||||||||| :::||||::| : | |||        :| :  :   :
Db      68 ISLLLIVTQDP-VSRICISKEAGEKMLPCKPYDGAGGGKGKDNHRRLLWLQGESETHRRF 126

Qy     111 ------VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWE 163
                 || |  :|||||| ||:||||:|||||||| |||:|: |||||: |||||
Db     127 LAAPAGVDVCAKQGKVALMSAGSMHQLHIFIFVLAVFHVLYSVVTMTLSRLKMKQWKKWE 186

Qy     164 TETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTL 223
           :|| |||||||||:| |||||: |:|||||||||:|||||||||| |||||||||
Db     187 SETASLEYQFANDPSRCRFTHQTTLVRRHLGLSSTPGVRWVVAFFRQFFTSVTKVDYLTL 246

Qy     224 RAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWI 283
           | |||||||||| ::|||||||||:|||||||| ||| || ||:| |||| :|:|||:|:
Db     247 RQGFINAHLSQGNRFDFHKYIKRSLEDDFKVVVRISLKLWFVAVLILFLDFDGIGTLLWM 306

Qy     284 SFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHL 343
           | :|||||| |||||||:||||| || || ||:|||| ||||||:|||:|||||||| :||
Db     307 SVVPLVILLWVGTKLEMVIMEMAQEIHDRESVVKGAPAVEPSNKYFWFNRPDWVLFLMHL 366

Qy     344 TLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQM 403
           |||||||||||||||||||||||| :: :|| |||:|:| | ||||:||||||||||||
Db     367 TLFQNAFQMAHFVWTVATPGLKKCYHEKMAMSIAKVVLGVAAQILCSYITFPLYALVTQM 426

Qy     404 GSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP 463
           ||:|||||||||:|||||||  |||||| ||  |||||| | ||         || ||||
Db     427 GSHMKRSIFDEQTAKALTNWRKMAKEKKKARDAAMLMAQMGGGAT--------PSVGSSP 478

Qy     464 VHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADI 523
           ||||||   ||||||| | ||| ::|        | ||  :: | |  ||||| ||:| |
Db     479 VHLLHKAGARSDDPQSVPASPRAEKEGGG-----VQHPARKVPPCDGWRSASSPALDAHI 533
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Qy     524 PSADFSFS 531
           | ||| ||
Db     534 PGADFGFS 541


RESULT   3
T03797
probable mlo protein - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 15-Jun-2001
C;Accession: T03797
R;Panstruga, R.
submitted to the EMBL Data Library, May 1997
A;Reference number: Z15093
A;Accession: T03797
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-537 <PAN>
A;Cross-references: EMBL:Z95353; PIDN:CAB08606.1
A;Experimental source: isolate IR-BB21
C;Genetics:
A;Gene: Mlo-h1
A;Introns: 42/3; 124/3; 163/3; 184/1; 213/3; 238/3; 268/2; 285/1; 298/3; 356/3; 368/3
C;Superfamily: barley pathogen resistance protein Mlo

  Query Match             64.3%;  Score 1792;  DB 2;  Length 537;
  Best Local Similarity   67.2%;  Pred. No. 3.5e-146;
  Matches  366;  Conservative   54;  Mismatches   85;  Indels   40;  Gaps   12;

Qy       9 ARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEAL----EKMKAEL 64
           :|||||||:|||||| | :|||| |||||| | |       |   | |        |||
Db       8 SRELPETPTWAVAVVCAVLVLVSAAMEHGLHNLSH------KTTAEVLIFLVLSALAEL 60

Qy      65 MLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE--------GRKPSKYV---DY 113
           ||:|||||||| | | | |:|||| : ||::: ||| | :          ||:       ||
Db      61 MLLGFISLLLTVAQAP-ISKICIPKSAANILLPCKAGQDAIEEEEAASGRRSLAGAGGGDY 119

Qy     114 CP--EGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEY 171
           |   :|||||||  |:||||:|||||||||||| :||: | |||||: |||||::| ||||
Db     120 CSKFDGKVALMSAKSMHQLHIFIFVLAVFHVTYCIITMGLGRLKMKKWKKWESQTNSLEY 179

Qy     172 QFANDPARFRFTHQTSFVKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINA 230
           ||| ||:|||||||||||||||  |||||:||:|||||||| |||||||||:| |||||
Db     180 QFAIDPSRFRFTHQTSFVKRHLGSFSSTPGLRWIVAFFRQFFGSVTKVDYLTMRQGFINA 239

Qy     231 HLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVI 290
           |||||||||||||||||:|||||||||||||| | || |||||:|:|||||||:||:|
Db     240 HLSQNSKFDFHKYIKRSLEDDFKVVVGISLPLWFVGILVLFLDIHGLGTLIWISFVPLII 299

Qy     291 LLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAF 350
           :| |||||||:|||||  ||||||:||:|||:|||||:|||:|||||||||||||| |||
Db     300 VLLVGTKLEMVIMEMAQEIQDRATVIQGAPMVEPSNKYFWFNRPDWVLFFIHLTLFHNAF 359

Qy     351 QMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRS 410
           ||||||||:|||||||:|  | |||::|:||::|| ||||:|||||||||||||||::
Db     360 QMAHFVWTMATPGLKKCFHENIWLSIVEVIVGISLQVLCSYITFPLYALVTQMGSNMKKT 419

Qy     411 IFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKG 470
           ||:||| ||| |||  | |||||||  |  :||| |      ::|  || :||||||
Db     420 IFEEQTMKALMNWRKKAMEKKKVRDADAFLAQMSVDF-----ATPASSRSASPVHLLQDH 474

Qy     471 MGRSDDPQSAPT--SPRTQQEARDMYPVVVAHPVHRL--NPNDRRRSASSSALEADIPSA 526
           |||||  |  |  ||   :|  |||||  |    :|  :| |||  ||||   |||  :
Db     475 RARSDDPPSPITVASPPAPEE--DMYPVPAAAASRQLLDDPPDRRWMASSS---ADIADS 529

Qy     527 DFSFS 531
           |||||
Db     530 DFSFS 534


RESULT   4
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B86247
hypothetical protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: B86247
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: B86247
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-573 <STO>
A;Cross-references: GB:AE005172; NID:g5734726; PIDN:AAD49991.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
C;Superfamily: barley pathogen resistance protein Mlo

Query Match 45.0%; Score 1253.5; DB 2; Length 573;
Best Local Similarity 44.1%; Pred. No. 9e-100;
Matches 261; Conservative 91; Mismatches 161; Indels 79; Gaps 13;

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Qy       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
Db       1 MADQ--VKERTLEETSTWAVAVVCFVLLFISIVLEHSIHKIGTWFKKKHKQALFEALEKV 58

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK----------- 109
Db      59 KAELMLLGFISLLLTIGQTP-ISNICISQKVASTMHPCSAAEEAKKYGKKDAGKKDDGDG 117

Qy     110 --------------YV----------DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTY 144
Db     118 DKPGRRLLLELAESYIHRRSLATKGYDKCAEKGKVAFVSAYGIHQLHIFIFVLAVVHVVY 177

Qy     145 SVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRW 203
Db     178 CIVTYAFGKIKMRTWKSWEEETKTIEYQYSNDPERFRFARDTSFGRRHLNFWSKTRVTLW 237

Qy     204 VVAFFRQFFRSVTKVDYLTLRAGFINAHLS--QNSKFDFHKYIKRSMEDDFKVVVGISLP 261
Db     238 IVCFFRQFFGSVTKVDYLALRHGFIMAHFAPGNESRFDFRKYIQRSLEKDFKTVVEISPV 297

Qy     262 LWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPV 321
Db     298 IWFVAVLFLLTNSYGLRSYLWLPFIPLVVILIVGTKLEVIITKLGLRIQEKGDVVRGAPV 357

Qy     322 VEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVV 381
Db     358 VQPGDDLFWFGKPRFILFLIHLVLFTNAFQLAFFAWSTYEFNLNNCFHESTADVVIRLVV 417

Qy     382 GLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMA 441
Db     418 GAVVQILCSYVTLPLYALVTQMGSKMKPTVFNDRVATALKKWHHTAKNETK-------HG 470

Qy     442 QMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHP 501
Db     471 RHSGSNTPFSSRPTTPTHGSSPIHLLHNFNNRS--VENYPSSPSPRYSGH-------GHH 521

Qy     502 VHRL-NPNDRRRSASSS-----ALEADIP--------------SADFSFSQ 532
Db     522 EHQFWDPESQHQEAETSTHHSLAHESSEPVLASVELPPIRTSKSLRDFSFKK 573
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RESULT 5
H96640

hypothetical protein T25B24.9 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: H96640
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: H96640
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-583 <STO>
A;Cross-references: GB:AE005173; NID:g4585879; PIDN:AAD25552.1; GSPDB:GN00141
C;Genetics:
A;Gene: T25B24.9
A;Map position: 1
C;Superfamily: barley pathogen resistance protein Mlo

Query Match 44.3%; Score 1234.5; DB 2; Length 583;
Best Local Similarity 43.6%; Pred. No. 4e-98;
Matches 261; Conservative 97; Mismatches 159; Indels 81; Gaps 12;

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Qy       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
Db       1 MADQ--VKEKTLEETSTWAVAVVCFVLLLISIVIEKLIHKIGSWFKKKNKKALYEALEKV 58

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRK---------- 106
Db      59 KAELMLMGFISLLLTIGQG-YISNICIPKNIAASMHPCSASEEARKYGKKDVPKEDEEEN 117

Qy     107 ------------------PSKYVDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVI 147
Db     118 LRRKLLQLVDSLIPRRSLATKGYDKCAEKGKVAFVSAYGMHQLHIFIFVLAVCHVIYCIV 177

Qy     148 TIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-WVVA 206
Db     178 TYALGKTKMRRWKKWEEETKTIEYQYSHDPERFRFARDTSFGRRHLSFWSKSTITLWIVC 237

Qy     207 FFRQFFRSVTKVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWG 264
Db     238 FFRQFFRSVTKVDYLTLRHGFIMAHLAPGSDARFDFRKYIQRSLEEDFKTIVEINPVIWF 297

Qy     265 VAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEP 324
Db     298 IAVLFLLTNTNGLNSYLWLPFIPFIVILIVGTKLQVIITKLGLRIQEKGDVVKGTPLVQP 357

Qy     325 SNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLA 384
Db     358 GDHFFWFGRPRFILFLIHLVLFTNAFQLAFFVWSTYEFGLKNCFHESRVDVIIRISIGLL 417

Qy     385 LQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMI 444
Db     418 VQILCSYVTLPLYALVTQMGSKMKPTVFNERVATALKSWHHTAKKNIKHGRTS------- 470

Qy     445 GDATPSRGSSPMPSRGSSPVHLL----HKGMGRSDDPQSAPTSPR----------TQQEA 490
Db     471 ESTTPFSSRPTTPTHGSSPIHLLRNAPHKRSRSVDESFANSFSPRNSDFDSWDPESQHET 530

Qy     491 RDMYPVVVAHPVH--RLNPNDRRRSASSSALE----------ADIPSADFSFSQ 532
Db     531 AE-----TSNSNHRSRFGEEESEKKFVSSSVELPPGPGQIRTQHEISTISLRDFSFKR 583
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RESULT 6
T02582

H. vulgare Mlo protein homolog [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 15-Jun-2001
C;Accession: T02582; D84814
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes,
submitted to the EMBL Data Library, August 1998
A;Description: Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence.
A;Reference number: Z14679
A;Accession: T02582
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-570 <ROU>
A;Cross-references: EMBL:AC004697; NID:g3402671; PID:g3402694
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: D84814
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-570 <STO>
A;Cross-references: GB:AE002093; NID:g3402694; PIDN:AAC28997.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g39200; T16B24.16
A;Map position: 2
A;Introns: 39/3; 59/1; 140/3; 179/3; 200/1; 229/3; 248/3; 280/2; 297/1; 310/3; 368/3; 38
C;Superfamily: barley pathogen resistance protein Mlo

Query Match 43.8%; Score 1220.5; DB 2; Length 570;
Best Local Similarity 45.3%; Pred. No. 6.2e-97;
Matches 254; Conservative 93; Mismatches 153; Indels 61; Gaps 12;

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Qy      7 VPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELML 66
          :  | | |||:||||||   :: :|:::|: || :|||||: :||||| |||||:||||||
Db      3 IKERSLEETPTWAVAVVCFVLLFISIMIEYFLHFIGHWFKKKHKKALSEALEKVKAELML 62

Qy     67 VGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE----------GRK--------- 106
          :|||||||:| | | :::|||  : |    ||    |          |||
Db     63 LGFISLLLVVLQTP-VSEICIPRNIAATWHPCSNHQEIAKYGKDYIDDGRKILEDFDSND 121

Qy    107 --------PSKYVDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR 157
                 :|  | | | |||||:|   :||||:||||||||||| | :|| || : ||:
Db    122 FYSPRRNLATKGYDKCAEKGKVALVSAYGIHQLHIFIFVLAVFHVLYCIITYALGKTKMK 181

Qy    158 TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSVT 216
          || || || ::|||:|||| ||||   ||| :||| : | :    |:      || |||
Db    182 KWKSWERETKTIEYQYANDPERFRFARDTSFGRRHLNIWSKSTFTLWI------FFGSVT 235

Qy    217 KVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDI 274
          |||||||| ||| |||   |  :||| |||:||:| || ||||||  :| :|:| :  :
Db    236 KVDYLTLRHGFIMAHLPAGSAARFDFQKYIERSLEQDFTVVVGISPLIWCIAVLFILTNT 295

Qy    275 NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRP 334
          :|  : :|: |:||:::| || ||:||| :: | ||::  |:||||||| :  ||| ||
Db    296 HGWDSYLWLPFLPLIVILIVGAKLQMIISKLGLRIQEKGDVVKGAPVVEPGDDLFWFGRP 355

Qy    335 DWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTF 394
          ::|| ||| || |||:| |||:     || |:| :     ::: :|: :| ||||:|
Db    356 RFILFLIHLVLFTNAFQLAFFVWSTYEFTLKNCFHHKTEDIAIRITMGVLIQVLCSYITL 415

Qy    395 PLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSS 454
          ||||||||||::|: :||::: : ||  | :|||:: |   :       |  ||
Db    416 PLYALVTQMGTSMRPTIFNDRVANALKKWHHTAKKQTKHGHS--------GSNTPHSSRP 467

Qy    455 PMPSRGSSPVHLLHKGMGRSDDPQ----SAPTSPRTQQEARDMYPVVVAHPVHRLNPNDR 510
            |: | |||||||    || | |    ::|: ||    :   :     |  |  :|  :
Db    468 TTPTHGMSPVHLLHNYNNRSLDQQTSFTASPSPPRFSDYSGQGH----GHQ-HFFDPESQ 522

Qy    511 RRSASSSALEADIPSADFSFS 531
```

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                |      : :|  ::|| |
Db    523 NHS-----YQREITDSEFSNS 538
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RESULT 7
B84748
similar to Mlo proteins from H. vulgare [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C;Accession: B84748
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: B84748
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-501 <STO>
A;Cross-references: GB:AE002093; NID:g6598814; PIDN:AAC69142.2; GSPDB:GN00139
C;Genetics:
A;Gene: At2g33670
A;Map position: 2
C;Superfamily: barley pathogen resistance protein Mlo

Query Match 39.5%; Score 1101.5; DB 2; Length 501;
Best Local Similarity 44.2%; Pred. No. 9.3e-87;
Matches 229; Conservative 88; Mismatches 140; Indels 61; Gaps 10;

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Qy      6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
            |  ||| :||:||| |   ::|:|:::|  :||:|  |  | ||||:|||:|:| |||
Db     11 GEGPRELDQTPTWAVSTVCGVIILISIVLELMIHKIGEVFTERRKKALYEALQKIKNELM 70

Qy     66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPC----KRGTEGRKP--SKYVD------- 112
          ::|||||||   |:  || :|::       |  |         | :||  :::::
Db     71 VLGFISLLLTFGQN-YIASLCVASRYGHAMSFCGPYDGPSGESKKPKTTEHLERRVLADA 129

Qy    113 ---YCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSL 169
              | :| | |:|  :|||:|:||| |||||| || ||: | | |:| || || |  :
Db    130 APAQCKKGYVPLISLNALHQVHIFIFFLAVFHVIYSAITMMLGRAKIRGWKVWEEEVIN- 188

Qy    170 EYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-----WVVAFFRQFFRSVTKVDYLTLR 224
          :::  |||:||| ||:|||: |:     |  :     :|: |||  ||| | ||||:|
Db    189 DHEMMNDPSRFRLTHETSFVREHV----NPWAKNRFSFYVMCFFRQMLRSVRKSDYLTMR 244

Qy    225 AGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWIS 284
          |||: ||:   ||:| ||||||:|||||||||||  ||   :| |  |::|      |:
Db    245 HGFISVHLAPGMKFNFQKYIKRSLEDDFKVVVGISPELWAFVMLFLLFDVHGWYVTAVIT 304

Qy    285 FIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLT 344
          || :: | :|||: || :||||||:| :||:| |:|  |:: ||| ||  ||  ||
Db    305 MIPPLLTLAIGTKLQAIISDMALEIQERHAVIQGMPLVNVSDRHFWFSRPALVLHIIHFI 364

Qy    345 LFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMG 404
          ||||||:: :| |     ||: |:|    | |::| :|: :|||||:| ||||||||||
Db    365 LFQNAFEITYFFWIWYEFGLRSCFHHHFALIIIRVALGVGVQFLCSYITLPLYALVTQMG 424

Qy    405 SNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPS------ 458
          | ||||:||:|||||| ||   ||:| :                || :   |:|:
Db    425 STMKRSVFDDQTSKALKNWHKNAKKKSE--------------TPGQTQPPLPNLRPKTG 469

Qy    459 ---RGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDM 493
              :|| ::            |       | ::||:
Db    470 GDIESASPANI----------TASVDVKESDQSQSRDL 497
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RESULT 8
F84552
similar to Mlo proteins from H. vulgare [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001

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C;Accession: F84552
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: F84552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-574 <STO>
A;Cross-references: GB:AE002093; NID:g4914369; PIDN:AAD32905.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g17480
A;Map position: 2
C;Superfamily: barley pathogen resistance protein Mlo


  Query Match             39.0%;  Score 1088;  DB 2;  Length 574;
  Best Local Similarity   42.6%;  Pred. No. 1.6e-85;
  Matches  245;  Conservative   86;  Mismatches  152;  Indels   92;  Gaps   14;

Qy       3 DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62
           |:| |  ::| :||:|||| |    ::|||||:|  |||:|     ||| || :||||:||
Db      32 DEKKVVHKQLNQTPTWAVAAVCTFFIVVSVLLEKLLHKVGKVLWDRHKTALLDALEKIKA 91

Qy      63 ELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPC----------KRGTEGRK------ 106
           |||::|||||||   |  |:  |||    |  | ||          |   |:
Db      92 ELMVLGFISLLLTFGQTYIL-DICIPSHVARTMLPCPAPNLKKEDDDNGESHRRLLSFEH 150

Qy     107 ---------PSKYVDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKM 156
                    |:|    |  || | |:|  :|||||: || ||:||| || :|: | |||:
Db     151 RFLSGGEASPTK----CTKEGYVELISAEALHQLHILIFFLAIFHVLYSFLTMMLGRLKI 206

Qy     157 RTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSV 215
           | || || ||:|  |:|: | :||| ||:|||: |    :  |   :|  |||||||||
Db     207 RGWKHWENETSSHNYEFSTDTSRFRLTHETSFVRAHTSFWTRIPFFFYVGCFFRQFFRSV 266

Qy     216 TKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDIN 275
            : |||||| |||  ||:  |:|:| |||||:||||||||:|  |||  :| | |:|:
Db     267 GRTDYLTLRNGFIAVHLAPGSQFNFQKYIKRSLEDDFKVVVGVSPVLWGSFVLFLLLNID 326

Qy     276 GVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPD 335
                               |||| |:  ||| | || :|::| |:|: :::|||| ||
Db     327 ------------------GTKLQAIMTRMALGITDRHAVVQGMPLVQGNDEYFWFGRPH 367

Qy     336 WVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFP 395
            :|  :|  |||||||: :| |   : |   |||    ::::|| : | :  ||||:| |
Db     368 LILHLMHFALFQNAFQITYFFWIWYSFGSDSCYHPNFKIALVKVAIALGVLCLCSYITLP 427

Qy     396 LYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSP 455
           |||||||||| ||:|:|||||||||  ||   |:|| |: |   :    || : |  :|
Db     428 LYALVTQMGSRMKKSVFDEQTSKALKKWRMAVKKKKGVKATTKRLG---GDGSASPTAST 484

Qy     456 MPSRGS---------SPVHLLHKGMGRSDDPQSA----------PTSPRTQQEARDMYP 495
           : | |          :|  : ::|:    ||:::           | || :       :
Db     485 VRSTSSVRSLQRYKTTPHSMRYEGL----DPETSDLDTDNEALTPPKSPPS-------FE 533

Qy     496 VVVAHPVHRLNPNDRRRSASSSALEADIPSADFSF 530
           :||     :: ||      :|   | |  | :|||
Db     534 LVV-----KVEPNKTNTGETSRDTETD--SKEFSF 561


RESULT   9
B84552
similar to Mlo proteins from H. vulgare [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C;Accession: B84552
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: B84552
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-580 <STO>
A;Cross-references: GB:AE002093; NID:g6598336; PIDN:AAB86520.2; GSPDB:GN00139
C;Genetics:
A;Gene: At2g17430
A;Map position: 2
C;Superfamily: barley pathogen resistance protein Mlo


  Query Match             38.1%;  Score 1061;  DB 2;  Length 580;
  Best Local Similarity   45.7%;  Pred. No. 3.5e-83;
  Matches  220;  Conservative   75;  Mismatches  130;  Indels   56;  Gaps    8;

Qy       6 GVPA--RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGH---------------------- 43
           | |:  :|| :||:||||||   ::|:| |:| || :| :
Db      25 GAPSGGKELSQTPTWAVAVVCTFLILISHLLEKGLQRLANVCFLLLLLLFLRVFLFKHSL 84

Qy      44 ----------WFQHRHKKALWEALEKMKAELMLVGFISLLLIVTQDPIIAKICISEDAAD 93
                     |   :|| :| |||||:|||||::|||||||    :| | |||:   ||
Db      85 SETYEFVSSQWLWKKHKNSLLEALEKIKAELMILGFISLLL-TFGEPYILKICVPRKAAL 143

Qy      94 VMWPC-KRGT---EGRKPSKYVDY----------CPEGKVALMSTGSLHQLHVFIFVLAV 139
           | ||    |   :   ||    :           | :|   |::   |||||: :| ||:
Db     144 SMLPCLSEDTVLFQKLAPSSLSRHLLAAGDTSINCKQGSEPLITLKGLHQLHILLFFLAI 203

Qy     140 FHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SST 198
           ||: ||:||: |||||:| ||||| || | :|:|: | :| | ||:||||: |    ::|
Db     204 FHIVYSLITMMLSRLKIRGWKKWEQETLSNDYEFSIDHSRLRLTHETSFVREHTSFWTTT 263

Qy     199 PGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGI 258
           |   :|  |||||| || : |||||| |||:|||:   ||:| :|||||:|||||:||||
Db     264 PFFFYVGCFFRQFFVSVERTDYLTLRHGFISAHLAPGRKFNFQRYIKRSLEDDFKLVVGI 323

Qy     259 SLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKG 318
           |  ||   :: |  ::||  || | |  ||:|:| |||||: |:  |||||  :  :|::|
Db     324 SPVLWASFVIFLLFNVNGWRTLFWASIPPLLIILAVGTKLQAIMATMALEIVETHAVVQG 383

Qy     319 APVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMK 378
           |:|: |:::|||  |  :|  ||  |||||||: || |   : ||| |:|    | : |
Db     384 MPLVQGSDRYFWFDCPQLLLHLIHFALFQNAFQITHFFWIWYSFGLKSCFHKDFNLVVSK 443

Qy     379 VVVGLALQFLCSYMTFPLYALVT--------QMGSNMKRSIFDEQTSKALTNWRNTAKEK 430
           : : |    ||||:| |||||||         ||||:||:::|||| :|||  |    | |
Db     444 LFLCLGALILCSYITLPLYALVTQMMKWCVEQMGSHMKKAVFDEQMAKALKKWHKDIKLK 503

Qy     431 K 431
           |
Db     504 K 504


RESULT  10
E96495
hypothetical protein F8D11.2 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: E96495
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: E96495
A;Status: preliminary
```

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A;Molecule type: DNA
A;Residues: 1-443 <STO>
A;Cross-references: GB:AE005173; NID:g10092398; PIDN:AAG12804.1; GSPDB:GN00141
C;Genetics:
A;Gene: F8D11.2
A;Map position: 1
C;Superfamily: barley pathogen resistance protein Mlo


  Query Match           37.6%;  Score 1049;  DB 2;  Length 443;
  Best Local Similarity  48.8%;  Pred. No. 2.6e-82;
  Matches  218;  Conservative   66;  Mismatches  129;  Indels   34;  Gaps    6;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |   |:| :||:|||: |   ::|:|:|:::|  :||:|  |: : ||||:|||||:| |||
Db      10 GEGPRQLDQTPTWAVSTVCGVIILISIILELIIHKVGEVFERKKKKALFEALEKIKNELM 69

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPC----KRGTEGRKPSKYVDY-------- 113
           ::|||||||   |:  || ||:       | |        : ||  |  |:
Db      70 VLGFISLLLTFGQN-YIASICVPSRYGHAMSFCGPYDGPSEDDRKKLKKTDHAMRILYSV 128

Qy     114 -------CPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETET 166
                 |   |||:|  :|||:|:|||  |||||| || ||: | | |:| || || |
Db     129 QRRSLADAPPDYVALISLNALHQVHIFIFFLAVFHVIYSAITMMLGRAKIRGWKVWEQEV 188

Qy     167 TSLEYQFANDPARFRFTHQTSFVKRHL-GLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRA 225
             | :  |||:||| ||:|||| |:   :|     :|: |||  ||| | ||||:|
Db     189 IH-EQEMMNDPSRFRLTHETSFVREHVNSWASNKFFFYVMCFFRQILRSVRKSDYLTMRH 247

Qy     226 GFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISF 285
           |||: ||:   |||| ||||||:|||||||||   ||   :| |  |::|      |:
Db     248 GFISVHLAPGMKFDFQKYIKRSLEDDFKVVVGIRPELWAFVMLFLLFDVHGWYVTAVITM 307

Qy     286 IPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTL 345
           || :: | :|||: ||  |||||:| :||:| |||  |:: ||| :|| ||  ||  |
Db     308 IPPLLTLAIGTKLQAIISYMALEIQERHAVIQGMPVVNVSDQHFWFEKPDLVLHMIHFVL 367

Qy     346 FQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGS 405
           ||  |            ||: |:|   || |::| :|: :|||||:| ||||||||||
Db     368 FQYEF-----------GLRSCFHHHFGLIIIRVCLGVGVQFLCSYITLPLYALVTQMGS 415

Qy     406 NMKRSIFDEQTSKALTNWRNTAKEKKK 432
           ||||:|||||||||  |   |::| :
Db     416 TMKRSVFDEQTSKALEQWHKKARKKNE 442


RESULT  11
T01089
hypothetical protein T10P11.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 15-Jun-2001
C;Accession: T01089
R;Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bastide, M
hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R.
submitted to the EMBL Data Library, November 1998
A;Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A;Reference number: Z14248
A;Accession: T01089
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-526 <KAP>
A;Cross-references: EMBL:AC002330; NID:g2262135; PID:g3892049
A;Experimental source: cultivar Columbia
C;Genetics:
A;Map position: 4
A;Introns: 61/1; 145/3; 184/3; 205/1; 237/3; 262/3; 309/1; 322/3; 392/3; 415/2; 435/3
A;Note: T10P11.12
C;Superfamily: barley pathogen resistance protein Mlo


  Query Match           33.4%;  Score 932.5;  DB 2;  Length 526;
  Best Local Similarity  40.5%;  Pred. No. 3.5e-72;
  Matches  202;  Conservative   79;  Mismatches  167;  Indels   51;  Gaps   10;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |     |  ||:|  || |   :| :|: :|  ||  |   : : :|  |:|||:|:| |||
Db       4 GGEGMSLEFTPTWVVAGVCTVIVAISLAVERLLHYFGTVLKKKKQKPLYEALQKVKEELM 63

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCKR------------------------- 100
           |:|||||| | |  :|:| |: |:    | ||
Db      64 LLGFISLLLTVFQG-LISKFCVKENVLMHMLPCSLDSRREAGASEHKNVTAKEHFQTFLP 122

Qy     101 --GTEGRKPSKY----VDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSR 153
             ||  |  :::    | || | ||| |:|  :|| ||:||||||: |||: |:|:
Db     123 IVGTTRRLLAEHAAVQVGYCSEKGKVPLLSLEALHHLHIFIFVLAISHVTFCVLTVIFGS 182

Qy     154 LKMRTWKKWETETTSLEYQFANDP------ARFRFTHQTSFVKRH-LGLSSTPGI-RWVV 205
             ::  |||||      ::    ||       |    |  :|:| | ||:     |  |
Db     183 TRIHQWKKWEDSIADEKF----DPETALRKRRVTHVHNHAFIKEHFLGIGKDSVILGWTQ 238

Qy     206 AFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGV 265
           :| :||: |||| ||:||| |||  |   | | :||||: |::|||| ||||  ||
Db     239 SFLKQFYDSVTKSDYVTLRLGFIMTHCKGNPKLNFHKYMMRALEDDFKQVVGISWYLWIF 298

Qy     266 AILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPS 325
             :: | |::||  |  ||:|||  :|| |||||| :| ::| |: ::   |:|  ||:||
Db     299 VVIFLLLNVNGWHTYFWIAFIPFALLLAVGTKLEHVIAQLAHEVAEKHVAIEGDLVVKPS 358

Qy     326 NKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLAL 385
           :: ||| :|  ||: ||  |||||::| | |   | |   |   |:   : ::|:|: :
Db     359 DEHFWFSKPQIVLYLIHFILFQNAFEIAFFFWIWVTYGFDSCIMGQVRYIVPRLVIGVFI 418

Qy     386 QFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIG 445
           | |||| | ||||:|:|||||: |::||:|      | |    |:|:     |:  |  |
Db     419 QVLCSYSTLPLYAIVSQMGSSFKKAIFEENVQVGLVGWAQKVKQKR-----DLKAAASNG 473

Qy     446 DATPSR-GSSPMPSRGSSP 463
           |   |: | |    ||:|
Db     474 DEGSSQAGPGPDSGSGSAP 492


RESULT  12
T00691
H. vulgare Mlo protein homolog At2g44110 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein F6E13.24
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 15-Jun-2001
C;Accession: T00691; E84874
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke
submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence.
A;Reference number: Z14180
A;Accession: T00691
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-496 <ROU>
A;Cross-references: EMBL:AC004005; NID:g3212846; PID:g3212880
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: E84874
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-496 <STO>
A;Cross-references: GB:AE002093; NID:g3212880; PIDN:AAC23431.1; GSPDB:GN00139
C;Genetics:
A;Gene: F6E13.24; At2g44110
A;Map position: 2
A;Introns: 39/3; 59/1; 132/3; 171/3; 193/3; 222/3; 247/3; 277/2; 294/1; 307/3; 377/3;
C;Superfamily: barley pathogen resistance protein Mlo
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  Query Match             33.2%;  Score 927;  DB 2;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 9.7e-72;
  Matches  205;  Conservative   89;  Mismatches  168;  Indels   52;  Gaps   11;

Qy      12 LPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGFIS 71
           |  ||:| ||:| : :| :|  :|  :|: |  |::  :| |: ||:|:| ||||||||| 
Db       8 LEYTPTWVVALVCSVIVSISFAVERLIHRAGKHFKNNDQKQLFGALQKIKEELMLVGFIS 67

Qy      72 LLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK--------------------YV 111
           ||| | |   |||||||:: ::   || :     |  |                     
Db      68 LLLSVGQSK-IAKICISKELSEKFLPCTKPAGAEKSLKDSSHFQFSFTGRHLLAGDAPAG 126

Qy     112 DYCP-EGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLE 170
           |||  :||| :||  :||:|||:||||||| |: : ::||    :|:: ||||| :   ||  
Db     127 DYCSLKGKVPIMSLSALHELHIFIFVLAVAHIIFCLLTIVFGTMKIKQWKKWEDKV--LE 184

Qy     171 YQFANDPARFRFTH--QTSFVK-RHLGL-SSTPGIRWVVAFFRQFFRSVTKVDYLTLRAG 226
             |  | :  :|||  :  |:: | ||:  :   : || :| :||  || : ||:|:| | 
Db     185 KDFDTDQSIKKFTHVQEHEFIRSRFLGVGKADASLGWVQSFMKQFLASVNESDYITMRLG 244

Qy     227 FINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFI 286
           |:  |    | ||:||||: |::  ||| |||||  ||   :| | |:|       |::||
Db     245 FVTTHCKTNPKFNFHKYLMRALNSDFKKVVGISWYLWVFVVLFLLLNIVAWHVYFWLAFI 304

Qy     287 PLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLF 346
           ||::|| |||||| || ::| |: ::   ::|  || ||:  |||  |  ||| ||  ||  
Db     305 PLILLLAVGTKLEHIITDLAHEVAEKHIAVEGDLVVRPSDDLFWFQSPRLVLFLIHFILF 364

Qy     347 QNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSN 406
           ||:|::|:| : :   |   |    :   | ::|:|: :| |||| | ||||||||||:  
Db     365 QNSFEIAYFFFILFQFGWDSCIMDHVKFVIPRLVIGVIIQLLCSYSTLPLYALVTQMGSS 424

Qy     407 MKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHL 466
           | :||:||| : |  |   ||  |  | : :    ||| | |  : |       |      
Db     425 FKGAIFNEQTQEHLVGWAKMAKRGVKKGATQVGTSH---DATSPRPSIQLNS-------L 474

Qy     467 LHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAH 500
           | ||  : :       :|: : |        :||  
Db     475 LGKGSSQQNQ------NPKEKSE--------IAH 494


RESULT  13
T09888
hypothetical protein T22A6.80 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Jun-2001
C;Accession: T09888
R;Bevan, M.; Zimmermann, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; May
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16896
A;Accession: T09888
A;Molecule type: DNA
A;Residues: 1-429 <BEV>
A;Cross-references: EMBL:AL078637; GSPDB:GN00062; ATSP:T22A6.80
A;Experimental source: cultivar Columbia; BAC clone T22A6
C;Genetics:
A;Gene: ATSP:T22A6.80
A;Map position: 4
A;Introns: 40/3; 60/1; 87/3; 126/3; 151/3; 177/3; 202/3; 232/2; 262/3; 331/3; 354/2; 374
C;Superfamily: barley pathogen resistance protein Mlo


  Query Match             30.6%;  Score 853.5;  DB 2;  Length 429;
  Best Local Similarity   41.8%;  Pred. No. 1.7e-65;
  Matches  181;  Conservative   70;  Mismatches  149;  Indels   33;  Gaps    6;

Qy      12 LPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGFIS 71
           |  ||:| || :   :||:|:| | ||| ||   : | : ||:|||:|:| ||||:||||
Db       9 LEYTPTWVVAFICFIIVLLSLLAERGLHHLGKCLKRRQQDALFEALQKLKEELMLLGFIS 68

Qy      72 LLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVALMSTGSLHQLH 131
           |:| |:|   |  ||:                  |:      |:| |:|  :|||||
Db      69 LMLTVSQ-AAIRHICV------------------PPAL-------GQVPLVSVEALHQLH 102

Qy     132 VFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKR 191
           :|||||||||| :   |: |   ::: || ||         |     :   |:    | :
Db     103 IFIFVLAVFHVIFCASTMVLGGARIQQWKHWEDWFKKRPSQKGERDSTILFSANHEFFEM 162

Qy     192 HLG--LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSME 249
           | |     :  | || :||:||: |||| :|: ||  || :|   |  ||||||: |::|  
Db     163 HAGGFWRRSVVISWVRSFFKQFYGSVTKSEYIALRQAFIMSHCRTNPSFDFHKYMLRTLE 222

Qy     250 DDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEI 309
           |||  || ||  ||   :: | |:: |  |  |:||:||::|| || ||| ||  :||::  
Db     223 IDFKKVVSISWYLWLFVVVFLLLNVGGWNTYFWLSFLPLILLLMVGAKLEYIISSLALDV 282

Qy     310 QDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYH 369
           ::|  : | |: ||:: ||||||  ||  ||  ||||:|::| | | : | |:  |     
Db     283 SEKRSRAEEA-VITPSDELFWFHRPGIVLQLIHFILFQNSFEIAFFFWILFTYGIHSCIM 341

Qy     370 TQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNW----RN 425
           ::|  | ::|:|: :| |||| | ||||||||||  |: |||      |  |    ||  
Db     342 EKLGYLIPRLVMGVLVQVLCSYSTLPLYALVTQMGSKFKKGIFDNVVQSTLEGWLEDTRN 401

Qy     426 TAKEKKKVRDTDM 438
             :   :    :|  
Db     402 RGESTSEAHRIEM 414


RESULT  14
T47469
hypothetical protein F18N11.50 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 15-Jun-2001
C;Accession: T47469
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke,
submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24467
A;Accession: T47469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-485 <JOR>
A;Cross-references: EMBL:AL132953
A;Experimental source: cultivar Columbia; BAC clone F18N11
C;Genetics:
A;Map position: 3
A;Introns: 50/3; 70/1; 137/3; 176/3; 205/2; 225/3; 255/2; 272/1; 285/3; 343/3; 355/3;
A;Note: F18N11.50
C;Superfamily: barley pathogen resistance protein Mlo


  Query Match             28.4%;  Score 790.5;  DB 2;  Length 485;
  Best Local Similarity   37.3%;  Pred. No. 5.4e-60;
  Matches  177;  Conservative   90;  Mismatches  158;  Indels   49;  Gaps    9;

Qy      10 RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGF 69
           | | |||:||:| |    : ||: :|  :: |    :  | :| ||:||:|: ||::||
Db      17 RSLQETPTWALATVCFFFIAVSICLERLINLLSTRLKKNRKTSLLEAVEKLKSVLMVLGF 76

Qy      70 ISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRK-------------PSKYVDYC- 114
           :||:| ||:   ::||||    |: | ||::  :                 : :   |  
Db      77 MSLMLNVTEGE-VSKICIPIKYANRMLPCRKTIKSHNDVSEDDDDDDGDNHDNSFFHQCS 135

Qy     115 PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFA 174
           :|| :|:|   | ||  | |||| |:  ::  : |   |   :     |   :|:      
Db     136 SKGKTSLISEEGLTQLSYFFFVLACMHILCNLAILLLGMAKFFVYVIHIDE--KMEFVGE 193

Qy     175 NDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQ 234
           ||              : |:||:          |||: || |||||||| ||| ||:|  
Db     194 RDP--------------NSGVSSSK---------RQFYNSVAKVDYLTLRHGFIFAHVSS 230

Qy     235 NSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCV 294
           |: |:|  ||:||: :||| |||||  :|   :: : ||::|     ::||:||:|:| : 
Db     231 NNAFNFQNYIQRSLHEDFKTVVGISPLMWLTVVIFMLLDVSGWRVYFYMSFVPLIIVLVI 290

Qy     295 GTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAH 354
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Jun-2001
C;Accession: H86393
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
A;Accession: H86393
A;Status: preliminary
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C;Superfamily: barley pathogen resistance protein Mlo


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Date: Jul 23, 2002  3:36 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

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VERSION     A92828.1  GI:6741365
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1602)
  AUTHORS   Panstruga,R. and Bueschges,R.
  TITLE     POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
            PLANTS
  JOURNAL   Patent: WO 9804586-A 2 05-FEB-1998;
            INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES             Location/Qualifiers
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VERSION     A92833.1  GI:6741370
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            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1917)
  AUTHORS   Panstruga,R. and Bueschges,R.
  TITLE     POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
            PLANTS
  JOURNAL   Patent: WO 9804586-A 7 05-FEB-1998;
            INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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1525 GAGACACGGACATGCTGATGGCTCAGATGATCGGCGACGCAACACCGAGC 1574

 451 ArgGlySerSerProMetProSerArgGlySerSerProValHisLeuLe 467
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    1725 CCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTC 1774

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seq_documentation_block:
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DEFINITION  H.vulgare mRNA for Mlo protein.
ACCESSION   Z83834
VERSION     Z83834.1  GI:1877220
KEYWORDS    Mlo gene.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1917)
  AUTHORS   Bueschges,R., Hollricher,K., Panstruga,R., Simons,G., Wolter,M.,
            Frijters,A., van Daelen,R., van de Lee,T., Diergaarde,P.,
            Groenendijk,J., Toepsch,S., Vos,P., Salamini,F. and
            Schulze-Lefert,P.
  TITLE     The barley Mlo gene: a novel control element of plant pathogen
            resistance
  JOURNAL   Cell 88 (5), 695-705 (1997)
  MEDLINE   97207016
REFERENCE   2  (bases 1 to 1917)
  AUTHORS   Panstruga,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury
            Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK
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BASE COUNT      395 a    576 c    553 g    393 t
ORIGIN


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alignment_block:
 US-09-722-377-1 x HVMLO   ..

 Align seg 1/1  to: HVMLO  from: 1  to: 1917

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     325 TGGAACACGGCCTCCACAAGCTCGGCCATTGGTTCCAGCACCGGCACAAG 374

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      67 lGlyPheIleSerLeuLeuLeuIleValThrGlnAspProIleIleAlaL 84
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     134 lePheValLeuAlaValPheHisValThrTyrSerValIleThrIleAla 150
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     267 eLeuThrLeuPheLeuAspIleAsnGlyValGlyThrLeuIleTrpIleS 284
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Date: Jul 23, 2002  3:41 PM

About: Results were produced by the GenCore software, version 4.5,
       Copyright (c) 1993-2000 Compugen Ltd.

Command line parameters:
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 -FGAPOP=6.000 -FGAPEXT=7.000 -YGAPOP=60.000 -YGAPEXT=60.000
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Search information block:
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Query length: 533
Database: N_Geneseq_032802:*
Database sequences: 1736436
Database length: 858457221
Search time (sec): 208.380000

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AC   AAV35022;
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DT   13-OCT-1998  (first entry)
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XX
KW   Barley; MLO; mildew; pathogen; resistance; ss.
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PD   05-FEB-1998.
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XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   P-PSDB; AAW59442.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Claim 2; Fig 2; 150pp; English.
XX
CC   The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC   regulatory function on a pathogen defence response, such that mutants
CC   exhibit a defence response in the absence of pathogen.  Down-regulation
CC   or out-competition of Mlo function may be used to stimulate a defence
CC   response in transgenic plants conferring increased pathogen resistance,
CC   especially resistance to powdery mildew or rust. The product can also
CC   be used for identifying compounds able to stimulate a defence response
CC   in a plant by interaction with encoded polypeptide.
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SQ   Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;


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 451 ArgGlySerSerProMetProSerArgGlySerSerProValHisLeuLe 467
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1351 CGAGGCTCGTCGCCGATGCCGAGCCGGGGCTCATCACCCGTGCACCTGCT 1400

 467 uHisLysGlyMetGlyArgSerAspAspProGlnSerAlaProThrSerP 484
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1401 TCACAAGGGCATGGGGCGGTCGGACGACCCCCAGAGCGCGCCCACCTCGC 1450

 484 roArgThrGlnGlnGluAlaArgAspMetTyrProValValValAlaHis 500
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 501 ProValHisArgLeuAsnProAsnAspArgArgArgSerAlaSerSerSe 517
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 517 rAlaLeuGluAlaAspIleProSerAlaAspPheSerPheSerGlnGly 533
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seq_documentation_block:

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ID   AAV35026 standard; cDNA; 1917 BP.
XX
AC   AAV35026;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO gene.
XX
KW   Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS   Hordeum vulgare.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= MLO protein
FT   polyA_signal    1890..1895
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XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
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PF   29-JUL-1997;   97WO-GB02046.
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PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   P-PSDB; AAW59443.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Disclosure; Fig 7; 150pp; English.
XX
CC   The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC   regulatory function on a pathogen defence response, such that mutants
CC   exhibit a defence response in the absence of pathogen.  Down-regulation
CC   or out-competition of Mlo function may be used to stimulate a defence
CC   response in transgenic plants conferring increased pathogen resistance,
CC   especially resistance to powdery mildew or rust. The product can also
CC   be used for identifying compounds able to stimulate a defence response
CC   in a plant by interaction with encoded polypeptide.
XX
SQ   Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;
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      67 lGlyPheIleSerLeuLeuLeuIleValThrGlnAspProIleIleAlaL 84
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      84 ysIleCysIleSerGluAspAlaAlaAspValMetTrpProCysLysArg 100
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     134 lePheValLeuAlaValPheHisValThrTyrSerValIleThrIleAla 150
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     284 erPheIleProLeuValIleLeuLeuCysValGlyThrLysLeuGluMet 300
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     317 sGlyAlaProValValGluProSerAsnLysPhePheTrpPheHisArgP 334
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     484 roArgThrGlnGlnGluAlaArgAspMetTyrProValValValAlaHis 500
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:34:36 ; Search time 212.74 Seconds
(without alignments)
12928.913 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcggacaaaaaaggggt.....tttccttcagccagggatga 1602

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 300

Total number of hits satisfying chosen parameters: 3

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1602	100.0	1602	19	AAV35022	Hordeum vulgare cv
2	1551	96.8	1917	19	AAV35026	Hordeum vulgare ML
3	399	24.9	2425	19	AAV35025	Hordeum vulgare ML

ALIGNMENTS

RESULT 1

AAV35022
ID AAV35022 standard; DNA; 1602 BP.
XX
AC AAV35022;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare cv. Ingrid MLO gene.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX
FH Key Location/Qualifiers
FT CDS 1..1602
FT /*tag= a
FT /product= MLO protein
XX
PN WO9804586-A2.
XX
PD 05-FEB-1998.
XX
PF 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
DR WPI; 1998-159149/14.
DR P-PSDB; AAW59442.
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Claim 2; Fig 2; 150pp; English.
XX
CC The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of Mlo function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX
SQ Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;

Query Match 100.0%; Score 1602; DB 19; Length 1602;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    301 ggcaccgagggccgcaagcccagcaagtacgttgactactgcccggagggcaaggtggcg 360
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Qy    421 catgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaag 480
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Qy    601 atcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactac 660
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Qy    781 ccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctc 840
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Qy    841 atctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatg 900
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Qy    901 atcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcccccc 960
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RESULT 2
AAV35026
ID AAV35026 standard; cDNA; 1917 BP.
XX
AC AAV35026;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX

FH	Key	Location/Qualifiers
FT	CDS	225..1826
FT		/*tag= a
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XX
PN WO9804586-A2.
XX
PD 05-FEB-1998.
XX
PF 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
DR WPI; 1998-159149/14.
DR P-PSDB; AAW59443.
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure; Fig 7; 150pp; English.
XX
CC The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of Mlo function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX

```
SQ   Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;

  Query Match             96.8%;  Score 1551;  DB 19;  Length 1917;
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  Matches 1601;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy     121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
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Qy     181 aaggcggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggacccc 240
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Qy     241 atcatcgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgc 300
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Qy     301 ggcaccgagggccgcaagcccagcaagtacgttgactactgcccggagggcaaggtggcg 360
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Qy     421 catgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaag 480
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Qy     481 aaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggttc 540
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Qy     541 cggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctggc 600
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Qy    1141 gtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtc 1200
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RESULT   3
AAV35025
ID   AAV35025 standard; DNA; 2425 BP.
XX
AC   AAV35025;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO gene homologue.
XX
KW   Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS   Hordeum vulgare.
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB02046.
XX
PR   07-MAR-1997;   97GB-0004789.
PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
XX
```

PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Disclosure; Fig 6; 150pp; English.
XX
CC The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of Mlo function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;

Query Match 24.9%; Score 399; DB 19; Length 2425;
Best Local Similarity 100.0%; Pred. No. 3.6e-184;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time: 6946 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 11:31:46 ; Search time 2110.63 Seconds
(without alignments)
15883.557 Million cell updates/sec

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Perfect score: 1602
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 300

Total number of hits satisfying chosen parameters: 6

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1602	100.0	1917	6	A92833	A92833 Sequence 7
3	1602	100.0	1917	8	HVMLO	Z83834 H.vulgare m
4	411	25.7	513	8	AF267999	AF267999 Triticum
5	399	24.9	2431	6	A92831	A92831 Sequence 5
6	399	24.9	59748	8	HVCH4H	Y14573 Hordeum vul

ALIGNMENTS

RESULT 1
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LOCUS A92828 1602 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 2 from Patent WO9804586.
ACCESSION A92828
VERSION A92828.1 GI:6741365
KEYWORDS .
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1602)
AUTHORS Panstruga,R. and Bueschges,R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN PLANTS
JOURNAL Patent: WO 9804586-A 2 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES Location/Qualifiers
source 1. .1602
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/clone="MLO"
BASE COUNT 336 a 488 c 466 g 312 t
ORIGIN

Query Match 100.0%; Score 1602; DB 6; Length 1602;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG 60

Qy      61 gcggtggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaag 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
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Qy   1201 acacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctc 1260
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Qy   1261 accaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatg 1320
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RESULT   2
A92833
LOCUS       A92833                 1917 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 7 from Patent WO9804586.
ACCESSION   A92833
VERSION     A92833.1  GI:6741370
KEYWORDS    .
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1917)
  AUTHORS   Panstruga,R. and Bueschges,R.
  TITLE     POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
            PLANTS
  JOURNAL   Patent: WO 9804586-A 7 05-FEB-1998;
            INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES             Location/Qualifiers
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BASE COUNT      395 a    576 c    553 g    393 t
ORIGIN


  Query Match           100.0%;  Score 1602;  DB 6;  Length 1917;
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Db    585 CTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGGTCTTC 644

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RESULT   3
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HVMLO
LOCUS       HVMLO                   1917 bp    mRNA    linear   PLN 07-MAR-1997
DEFINITION  H.vulgare mRNA for Mlo protein.
ACCESSION   Z83834
VERSION     Z83834.1  GI:1877220
KEYWORDS    Mlo gene.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1917)
  AUTHORS   Bueschges,R., Hollricher,K., Panstruga,R., Simons,G., Wolter,M.,
            Frijters,A., van Daelen,R., van de Lee,T., Diergaarde,P.,
            Groenendijk,J., Toepsch,S., Vos,P., Salamini,F. and
            Schulze-Lefert,P.
  TITLE     The barley Mlo gene: a novel control element of plant pathogen
            resistance
  JOURNAL   Cell 88 (5), 695-705 (1997)
  MEDLINE   97207016
REFERENCE   2  (bases 1 to 1917)
  AUTHORS   Panstruga,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury
            Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK
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ORIGIN
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  Best Local Similarity   100.0%;  Pred. No. 0;
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Db   1545 GCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGC 1604

Qy   1381 tcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcg 1440
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1605 TCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAGAGCGCG 1664

Qy   1441 cccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcac 1500
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   1501 ccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaa 1560
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Db   1725 CCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCGTCGTCGGCCCTCGAA 1784

Qy   1561 gccgacatccccagtgcagatttttccttcagccagggatga 1602
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Db   1785 GCCGACATCCCCAGTGCAGATTTTTCCTTCAGCCAGGGATGA 1826
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RESULT   4
AF267999
LOCUS       AF267999                513 bp    mRNA    linear   PLN 02-JUN-2001
DEFINITION  Triticum aestivum Mlo-like protein mRNA, partial cds.
ACCESSION   AF267999
VERSION     AF267999.1  GI:14279360
KEYWORDS    .
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 513)
  AUTHORS   Hu,D., Xie,W. and Zhao,G.
  TITLE     Triticum aestivum Mlo-like gene
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 513)
  AUTHORS   Hu,D., Xie,W. and Zhao,G.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-MAY-2000) Biotechnology Institute, Zhejiang
            University, 268 Kuaixuan Rd., Hangzhou, Zhejiang 310029, P. R.
            China
FEATURES             Location/Qualifiers
     source          1. .513
                     /organism="Triticum aestivum"
                     /cultivar="Huixianhong"
                     /db_xref="taxon:4565"
     CDS             <1. .>513
                     /codon_start=1
                     /product="Mlo-like protein"
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BASE COUNT      109 a    150 c    129 g    124 t      1 others
ORIGIN
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  Best Local Similarity   99.6%;  Pred. No. 1.1e-211;
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Qy    388 ctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccata 447
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Db      1 CTGCACGTCTTCATCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCATW 60

Qy    448 gctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctccttg 507
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Db     61 GCTCTAAGCCGTCTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCACCTCCTTG 120

Qy    508 gaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtg 567
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Db    121 GAATACCAGTTCGCAAATGATCCTGCACGGTTCCGGTTCACGCACCAGACGTCGTTCGTG 180

Qy    568 aagcgccacctgggcctctccagcacccctggcatcagatgggtggtggccttcttcagg 627
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Db    181 AAGCGCCACCTGGGCCTCTCCAGCACCCCTGGCATCAGATGGGTGGTGGCCTTCTTCAGG 240

Qy    628 cagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaac 687
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Db    301 GCGCATTTGTCGCAAAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTCGATGGAG 360

Qy    748 gacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctcacc 807
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Db    361 GACGACTTCAAGGTCGTCGTCGGCATCAGCCTCCCGCTGTGGGGTGTGGCGATCCTCACC 420

Qy    808 ctcttccttgacatcaatggggttggcacgctcatctggatttctttcatccctctcgtg 867
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Qy    868 atcctcttgtgtgttggaaccaagctggagatg 900
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Db    481 ATCCTCTTGTGTGTTGGAACCAAGCTGGAGATG 513
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RESULT   5
A92831
LOCUS       A92831                  2431 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 5 from Patent WO9804586.
ACCESSION   A92831
VERSION     A92831.1  GI:6741368
KEYWORDS    .
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 2431)
  AUTHORS   Panstruga,R. and Bueschges,R.
  TITLE     POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
            PLANTS
  JOURNAL   Patent: WO 9804586-A 5 05-FEB-1998;
            INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES             Location/Qualifiers
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BASE COUNT      524 a    693 c    599 g    615 t
ORIGIN
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Qy   1264 aactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatggct 1323
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Db   2077 AACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATGGCT 2136

Qy   1324 cagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccgggggctca 1383
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Qy   1384 tcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgccc 1443
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Db   2197 TCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAGAGCGCGCCC 2256

Qy   1444 acctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcacccg 1503
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Db   2257 ACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCACCCG 2316

Qy   1504 gtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagcc 1563
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LOCUS       HVCH4H                  59748 bp    DNA     linear   PLN 25-MAR-1999
DEFINITION  Hordeum vulgare DNA for chromosome 4H.
ACCESSION   Y14573
VERSION     Y14573.1  GI:2894376
KEYWORDS    Mlo gene; oligosaccharyltransferase; ribophorin I; RING finger
            protein.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 59748)
  AUTHORS   Panstruga,R., Buschges,R., Piffanelli,P. and Schulze-Lefert,P.
  TITLE     A contiguous 60 kb genomic stretch from barley reveals molecular
            evidence for gene islands in a monocot genome
  JOURNAL   Nucleic Acids Res. 26 (4), 1056-1062 (1998)
  MEDLINE   98128007
REFERENCE   2  (bases 1 to 59748)
  AUTHORS   Panstruga,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-AUG-1997) R. Panstruga, Sainsbury Laboratory, John
            Innes Centre, Colney Norwich NR4 7UH, UK
COMMENT     Related entry: Z83834.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 24.9%; Score 399; DB 8; Length 59748;
Best Local Similarity 100.0%; Pred. No. 3e-205;
Matches 399; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy    1264 aactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatggct 1323
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Qy    1324 cagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggctca 1383
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Qy    1384 tcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgccc 1443
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Qy    1444 acctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcacccg 1503
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Db   13891 ACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCACCCG 13950

Qy    1504 gtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagcc 1563
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1602	100.0	1917	6	A92833	A92833 Sequence 7
3	1602	100.0	1917	8	HVMLO	Z83834 H.vulgare m
4	1316.8	82.2	1868	6	AX063294	AX063294 Sequence
5	1315.2	82.1	1730	8	AF361932	AF361932 Triticum
6	1314.8	82.1	1693	6	AX063296	AX063296 Sequence
7	1308.8	81.7	1721	8	AF384145	AF384145 Triticum
8	1305.6	81.5	1819	8	AF384144	AF384144 Triticum
9	1305.6	81.5	1886	6	AX063298	AX063298 Sequence
10	1119	69.9	1399	8	AF361933	AF361933 Triticum
11	940	58.7	1635	6	A92838	A92838 Sequence 12
12	863.8	53.9	1740	8	AF384030	AF384030 Oryza sat
13	813.4	50.8	1894	8	AF388195	AF388195 Oryza sat
14	812.4	50.7	1872	8	AY029312	AY029312 Zea mays
15	767.2	47.9	1611	6	A92837	A92837 Sequence 11
16	581	36.3	2431	6	A92831	A92831 Sequence 5
17	531	33.1	59748	8	HVCH4H	Y14573 Hordeum vul
18	511	31.9	513	8	AF267999	AF267999 Triticum
19	425.2	26.5	1815	8	AY029317	AY029317 Zea mays
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21	379	23.7	2030	8	AY029313	AY029313 Zea mays
22	335.4	20.9	1836	8	AF369571	AF369571 Arabidops
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24	312	19.5	1040	6	AR172603	AR172603 Sequence
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35	272	17.0	5751	8	HVMLOH1	Z95496 H.vulgare M
36	267.4	16.7	2011	8	AY054241	AY054241 Arabidops
37	263.8	16.5	2281	6	A92832	A92832 Sequence 6
38	258	16.1	1096	8	AF369570	AF369570 Arabidops
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40	239.4	14.9	2098	6	A92829	A92829 Sequence 3
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ALIGNMENTS

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LOCUS A92828 1602 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 2 from Patent WO9804586.
ACCESSION A92828
VERSION A92828.1 GI:6741365
KEYWORDS .
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1602)
AUTHORS Panstruga,R. and Bueschges,R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN PLANTS
JOURNAL Patent: WO 9804586-A 2 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES Location/Qualifiers
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RESULT   2
A92833
LOCUS       A92833                 1917 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 7 from Patent WO9804586.
ACCESSION   A92833
VERSION     A92833.1  GI:6741370
KEYWORDS    .
SOURCE      barley.
  ORGANISM  Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1917)
  AUTHORS   Panstruga,R. and Bueschges,R.
  TITLE     POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
            PLANTS
  JOURNAL   Patent: WO 9804586-A 7 05-FEB-1998;
            INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
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BASE COUNT      395 a    576 c    553 g    393 t
ORIGIN

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  Best Local Similarity  100.0%;  Pred. No. 2.9e-261;
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RESULT   3
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LOCUS       HVMLO                   1917 bp    mRNA    linear   PLN 07-MAR-1997
DEFINITION  H.vulgare mRNA for Mlo protein.
ACCESSION   Z83834
VERSION     Z83834.1  GI:1877220
KEYWORDS    Mlo gene.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 1917)
  AUTHORS   Bueschges,R., Hollricher,K., Panstruga,R., Simons,G., Wolter,M.,
            Frijters,A., van Daelen,R., van de Lee,T., Diergaarde,P.,
            Groenendijk,J., Toepsch,S., Vos,P., Salamini,F. and
            Schulze-Lefert,P.
  TITLE     The barley Mlo gene: a novel control element of plant pathogen
            resistance
  JOURNAL   Cell 88 (5), 695-705 (1997)
  MEDLINE   97207016
REFERENCE   2  (bases 1 to 1917)
  AUTHORS   Panstruga,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JAN-1997) Panstruga R., John Innes Centre, Sainsbury
            Laboratory, Colney Lane, Norwich, Norfolk, NR4 7UH, UK
FEATURES             Location/Qualifiers
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DEFINITION  Sequence 3 from Patent WO0078799.
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VERSION     AX063294.1  GI:12541084
KEYWORDS    .
SOURCE      Triticum sp.
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1868)
  AUTHORS   Salmeron,J.M., Weislo,L.J., Strawn,L.J., Kramer,C.M., Wang,H.X.,
            Vernooij,B.T., Levin,J.Z., Heifetz,P.B., Patton,D.A. and Que,Q.
  TITLE     Mlo-genes controlling diseases
  JOURNAL   Patent: WO 0078799-A 3 28-DEC-2000;
            Novartis AG (CH)
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RESULT   5
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DEFINITION  Triticum aestivum seven transmembrane-spanning protein (Mlo2) mRNA,
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ACCESSION   AF361932
VERSION     AF361932.1  GI:15290588
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SOURCE      bread wheat.
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REFERENCE   1  (bases 1 to 1730)
  AUTHORS   Devoto,A., Hartmann,A., Piffanelli,P., Elliott,C., Simmons,C.,
            Taramino,G., Goh,C.-S., Schulze-Lefert,P. and Panstruga,R.
  TITLE     Co-Evolution among intracellular domains and the C-terminus of the
            seven-transmembrane Mlo protein is suggested by a detailed
            computational analysis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1730)
  AUTHORS   Elliott,C.E. and Schulze-Lefert,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
            Center, Colney Lane, Norwich NR4 7UH, UK
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ORIGIN


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Db    1005 AAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTCATACACCTGACGCTATTC 1064

Qy    1039 cagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaa 1098
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Db    1065 CAGAACGCGTTTCAGATGGCACATTTCGTGTGGACAGTGGCCACGCCCGGCTTGAAGAAA 1124

Qy    1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158
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Db    1125 TGCTTCCATATGCACATCGGGCTGAGCATCATGAAGGTCGTGCTGGGGCTGGCTCTTCAG 1184

Qy    1159 ttcctctgcagctatatgaccttcccccctctacgcgctcgtcacacagatgggatcaaac 1218
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Qy   1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
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Qy   1279 gccaaggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgac 1338
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Qy   1339 gcaacaccgagccgaggctcgtcgccgatgccgagccggggctcatcacccgtgcacctg 1398
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Db   1365 GCGACGCCCAGCCGAGGGGCGTCGCCCATGCCTAGCCGGGGCTCGTCGCCAGTGCACCTG 1424

Qy   1399 cttcacaagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458
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Qy   1459 cagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaat 1518
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Qy   1519 cctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgca 1578
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Db   1545 CCTGCTGACAGGAGAAGGTCGGTCTCGTCGTCGGCACTCGATGTCGACATTCCCAGCGCA 1604

Qy   1579 gatttttccttcagccagggatga 1602
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RESULT   6
AX063296
LOCUS       AX063296               1693 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 5 from Patent WO0078799.
ACCESSION   AX063296
VERSION     AX063296.1  GI:12541086
KEYWORDS    .
SOURCE      Triticum sp.
  ORGANISM  Triticum sp.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1693)
  AUTHORS   Salmeron,J.M., Weislo,L.J., Strawn,L.J., Kramer,C.M., Wang,H.X.,
            Vernooij,B.T., Levin,J.Z., Heifetz,P.B., Patton,D.A. and Que,Q.
  TITLE     Mlo-genes controlling diseases
  JOURNAL   Patent: WO 0078799-A 5 28-DEC-2000;
            Novartis AG (CH)
FEATURES             Location/Qualifiers
     source          1. .1693
                     /organism="Triticum sp."
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                     KKWETETXSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTK
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     misc_feature    190. .228
                     /note="location of the amino acid sequence set forth in
                     SEQ ID No:1"
     misc_feature    1177. .1218
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                     SEQ ID No:2"
BASE COUNT      360 a    505 c    472 g    355 t      1 others
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ORIGIN

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  Query Match             82.1%;  Score 1314.8;  DB 6;  Length 1693;
  Best Local Similarity   89.7%;  Pred. No. 1e-212;
  Matches 1435;  Conservative    1;  Mismatches  158;  Indels    6;  Gaps    2;

Qy       6 ggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggt 65
           |||| |  |       |||||||||  ||||||||||||||||||  |||||||||||  |
Db       9 GGACTACGAGTACCCCCCGGCGCGGACGCTGCCGGAGACGCCGTCCTGGGCGGTGGCGCT 68

Qy      66 ggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcgg 125
           ||||||||||| |||| |  ||||||||||||| |||| ||||  ||||||||||||||
Db      69 CGTCTTCGCCGTCATGATCATCGTGTCCGTCCTCCTGGAGCACGCGCTCCACAAGCTCGG 128

Qy     126 ccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggc 185
           ||||||||||||  | ||||||||||| || |||  ||||||||||||||||||| || ||
Db     129 CCATTGGTTCCACAAGCGGCACAAGAACGCGCTGGCGGAGGCGCTGGAGAAGATCAAAGC 188

Qy     186 ggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcat 245
           |||||| |||||||||||| |||||  || |||||  |||  ||| ||||||||||    ||
Db     189 GGAGCTGATGCTGGTGGGGTTCATCTCGCTGCTGCTCGCCGTGACGCAGGACCC---AAT 245

Qy     246 cgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcac 305
           | ||  |||||||||||||||| | ||||||  | |||||  |||||||||  |   | |
Db     246 CTCCGGGATATGCATCTCCGAGAAGGCCGCCAGCATCATGCGGCCCTGCAGCCTGCCCCC 305

Qy     306 cgagggccgcaagcccagcaagtacgttgactactgccc---ggagggcaaggtggcgct 362
           |   |  ||||  ||  |  | |  ||||||||  |     ||||||||||  ||||
Db     306 TGGTTCCGTCAAGAGCAAGTACAAAGACTACTACTGCGCCAAAAAGGGCAAGGTGTCGCT 365

Qy     363 catgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttcca 422
           ||||||||||||||||||||||||||| ||| | |||||||||||||||| ||||||||
Db     366 AATGTCCACGGGCAGCTTGCACCAGCTCCACATGTTCATCTTCGTGCTCGCCGTCTTCCA 425

Qy     423 tgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaagaa 482
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Db     426 TGTCACCTACAGCGTCATCATCATGGCTCTAAGCCGTCTCAAAATGAGGACATGGAAGAA 485

Qy     483 atgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggttccg 542
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Db     486 ATGGGAGACAGAGACCGYCTCCTTGGAATACCAGTTCGCAAATGATCCTGCGCGGTTCCG 545

Qy     543 gttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctggcat 602
           |||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db     546 CTTCACGCACCAGACGTCGTTCGTGAAGCGTCACCTGGGCCTCTCCAGCACCCCCGGCAT 605

Qy     603 cagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactacct 662
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Db     606 CAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGGTCGGTCACCAAGGTGGACTACCT 665

Qy     663 gaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttcca 722
           |||  ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     666 CACCCTGAGGGCAGGCTTCATCAACGCGCATTTGTCGCATAACAGCAAGTTCGACTTCCA 725

Qy     723 caagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctccc 782
           |||||||||||||||| |||||||||||||||| |||||||| ||||||||||||||
Db     726 CAAGTACATCAAGAGGTCCATGGAGGACGACTTCAAAGTCGTCGTTGGCATCAGCCTCCC 785

Qy     783 gctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctcat 842
           |||||||  ||||||||||||||||||||||||||||||||  ||  | ||| | ||||||||||
Db     786 GCTGTGGTGTGTGGCGATCCTCACCCTCTTCCTTGATATTGACGGGATCGGCACGCTCAC 845

Qy     843 ctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatgat 902
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Db     846 CTGGATTTCTTTCATCCCTCTCGTCATCCTCTTGTGTGTTGGAACCAAGCTGGAGATGAT 905

Qy     903 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaagggggccccgt 962
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Db     906 CATCATGGAGATGGCCCTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCGCCCGT 965

Qy     963 ggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1022
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Db    966 GGTTGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTCAT 1025

Qy   1023 acacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccac 1082
          |||||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db   1026 ACACCTGACGCTGTTCCAGAATGCGTTTCAGATGGCACATTTCGTCTGGACAGTGGCCAC 1085

Qy   1083 gcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggt 1142
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Db   1086 GCCCGGCTTGAAGAAATGCTTCCATATGCACATCGGTCTGAGCATCATGAAGGTCGTGCT 1145

Qy   1143 ggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcac 1202
          |||||| ||||| |||||||||||||||||||| ||||||||||||||||||||||||||
Db   1146 GGGGCTGGCTCTTCAGTTCCTCTGCAGCTATATCACCTTCCCCCTCTACGCGCTCGTCAC 1205

Qy   1203 acagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcac 1262
          |||||||||||| |||||||||||||||||||||||||||||||||| |||||||||| ||
Db   1206 ACAGATGGGATCGAACATGAAGAGGTCCATCTTCGACGAGCAGACGGCCAAGGCGCTGAC 1265

Qy   1263 caactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatggc 1322
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1266 CAACTGGCGGAACACGGCCAAGGAGAAGAAGAAGGTCCGAGACACGGACATGCTGATGGC 1325

Qy   1323 tcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccgggggctc 1382
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Db   1326 GCAGATGATCGGCGACGCGACGCCCAGCCGAGGCACGTCGCCGATGCCTAGCCGGGCTTC 1385

Qy   1383 atcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgcc 1442
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RESULT   7
AF384145
LOCUS       AF384145                1721 bp    mRNA    linear   PLN 10-JUN-2001
DEFINITION  Triticum aestivum MLo1 protein mRNA, complete cds.
ACCESSION   AF384145
VERSION     AF384145.1  GI:14334168
KEYWORDS    .
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1721)
  AUTHORS   Yu,L., Niu,J.-S., Ma,Z.-Q., Chen,P.-D. and Liu,D.-J.
  TITLE     Cloning, characterization analysis and expression of MLo1 gene from
            wheat
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1721)
  AUTHORS   Yu,L., Niu,J.-S., Ma,Z.-Q., Chen,P.-D. and Liu,D.-J.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-2001) Key Laboratory of Crop Cytogenetics,
            Nanjing Agricultural University, Nanjing, Jiangsu, China
FEATURES             Location/Qualifiers
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                     /protein_id="AAK60567.1"
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                     KKWETETASLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGVRWVVASFRQFFRSVTK
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ORIGIN


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  Matches 1426;  Conservative    0;  Mismatches  152;  Indels    6;  Gaps    2;

Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
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Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
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Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
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Db    201 CGGCACAAGAACGCGCTGGCGGAGGCGCTGGAGAAGATCAAGGCGGAGCTCATGCTGGTG 260

Qy    202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261
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Db    261 GGCTTCATCTCGCTGCTGCTCGCCGTGACGCAGGACCC---CATCTCCGGGATATGCATC 317

Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
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Db    318 CCCGAGAAGGCCGCCAGCATCATGCGGCCCTGCAAGCTGCCCCCTGGCTCCGTCAAGAGC 377

Qy    322 agcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcagc 378
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Db    378 AAGTACAAAGACTACTACTGCGCCAAACAGGGCAAGGTGTCGCTCATGTCCACGGGCAGC 437

Qy    379 ttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtc 438
          |||||||||||||| | ||||||||||||||| ||||||||||||||||||||||||||
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Qy    439 atcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagacc 498
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Qy    499 acctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacg 558
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Qy    559 tcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatgggtggtggcc 618
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Qy    619 ttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggc 678
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Qy    679 ttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagagg 738
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Qy    739 tcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcg 798
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Db    798 TCCATGGAGGACGACTTCAAAGTCGTCGTTGGCATCAGCCTCCCGCTGTGGTGTGTGGCG 857

Qy    799 atcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatc 858
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Db    858 ATCCTCACCCTCTTCCTTGACATTGACGGGATCGGCACGCTCACCTGGATTTCTTTCATC 917

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Db    918 CCTCTCGTCATCCTCTTGTGTGTTGGAACCAAGCTGGAGATGATCATCATGGAGATGGCC 977

Qy    919 ctggagatccaggaccgggcgagcgtcatcaaggggggcccccgtggtcgagcccagcaac 978
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Db    978 CTGGAGATCCAGGACCGGGCGAGCGTCATCAAGGGGGCGCCCGTGGTTGAGCCCAGCAAC 1037

Qy    979 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttc 1038
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||| | |||
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Qy   1039 cagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaa 1098
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Db   1098 CAGAACGCGTTTCAGATGGCACATTTCGTGTGGACAGTGGCCACGCGCGGCTTGAAGAAA 1157

Qy   1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158
          |||| ||| | ||| |||||||||||||||||||||||| ||| ||||||| ||||| |||
Db   1158 TGCTTCCATATGCACATCGGGCTGAGCATCATGAAGGTCGTGCTGGGGCTGGCTCTTCAG 1217

Qy   1159 ttcctctgcagctatatgaccttcccctctacgcgctcgtcacacagatgggatcaaac 1218
          |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db   1218 TTCCTCTGCAGCTATATCACCTTCCCGCTCTACGCGCTCGTCACACAGATGGGATCAAAC 1277

Qy   1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
          |||||||||||||||||||||||||||||| |||||||||| || ||||||||||||||||
Db   1278 ATGAAGAGGTCCATCTTCGACGAGCAGACGGCCAAGGCGCTGACAAACTGGCGGAACACG 1337

Qy   1279 gccaaggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgac 1338
          |||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||||
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Qy   1339 gcaacaccgagccgaggctcgtcgccgatgccgagccggggctcatcacccgtgcacctg 1398
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Db   1398 GCGACGCCCAGCCGAGGGGCGTCGCCCATGCCTAGCCGGGGCTCGTCGCCAGTGCACCTG 1457

Qy   1399 cttcacaagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458
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Db   1458 CTTCACAAGGGCATGGGACGGTCCGACGATCCCCAGAGCACGCCAACCTCGCCAAGGGCC 1517

Qy   1459 cagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaat 1518
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Db   1518 ATGGAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCATCCAGTCCACAGACTAAAT 1577

Qy   1519 cctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgca 1578
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Db   1578 CCTGCTGACAGGAGAAGGTCGGTCTCGTCGTCGGCACTCGATGTCGACATTCCCAGCGCA 1637

Qy   1579 gatttttccttcagccagggatga 1602
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Db   1638 GATTTTTCCTTCAGCCAAGGATGA 1661


RESULT   8
AF384144
LOCUS       AF384144                1819 bp    mRNA    linear   PLN 10-JUN-2001
DEFINITION  Triticum aestivum MLo protein mRNA, complete cds.
ACCESSION   AF384144
VERSION     AF384144.1  GI:14334166
KEYWORDS    .
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1819)
  AUTHORS   Yu,L., Niu,J.-S., Ma,Z.-Q., Chen,P.-D. and Liu,D.-J.
  TITLE     Cloning, location and expression of MLo gene from wheat
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1819)
  AUTHORS   Yu,L., Niu,J.-S., Ma,Z.-Q., Chen,P.-D. and Liu,D.-J.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-MAY-2001) Key Laboratory of Crop Cytogenetics,
            Nanjing Agricultural University, Nanjing, Jiangsu, China
FEATURES             Location/Qualifiers
     source          1. .1819
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                     SRGTSPMPSRGSSPVHLLQKGMGRSDDPQSAPTSPRTMEEARDMYPVVVAHPVHRLNP
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BASE COUNT      374 a    552 c    525 g    368 t
ORIGIN


  Query Match             81.5%;  Score 1305.6;  DB 8;  Length 1819;
  Best Local Similarity   89.9%;  Pred. No. 3.6e-211;
  Matches 1424;  Conservative    0;  Mismatches  154;  Indels    6;  Gaps    2;

Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
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Db    227 CCGGCGCGGACGCTGCCGGAGACGCCGTCCTGGGCGGTGGCGCTGGTCTTCGCCGTCATG 286

Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
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Db    287 ATCATCGTCTCCGTCCTCCTGGAGCACGCGCTCCACAAGCTCGGCCATTGGTTCCACAAG 346

Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
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Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
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Qy    799 atcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatc 858
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Qy    919 ctggagatccaggaccgggcgagcgtcatcaaggggccccccgtggtcgagcccagcaac 978
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Db   1244 CAGAACGCGTTTCAGATGGCACATTTCGTGTGGACAGTGGCCACGCCCGGCTTGAAGGAC 1303

Qy   1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158
Db   1304 TGCTTCCATATGAACATCGGGCTGAGCATCATGAAGGTCGTGCTGGGGCTGGCTCTCCAG 1363

Qy   1159 ttcctctgcagctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaac 1218
Db   1364 TTCCTGTGCAGCTACATCACCTTCCCCCTCTACGCGCTAGTCACACAGATGGGATCAAAC 1423

Qy   1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
Db   1424 ATGAAGAGGTCCATCTTTGACGAGCAGACAGCCAAGGCGCTGACCAACTGGCGGAACACG 1483

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Db   1544 GCAACACCCAGCCGAGGCACGTCCCCGATGCCTAGCCGGGGCTCATCGCCGGTGCACCTG 1603

Qy   1399 cttcacaagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458
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Qy   1579 gatttttccttcagccagggatga 1602
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RESULT   9
AX063298
LOCUS       AX063298                1886 bp    DNA     linear   PAT 24-JAN-2001
DEFINITION  Sequence 7 from Patent WO0078799.
ACCESSION   AX063298
VERSION     AX063298.1  GI:12541088
KEYWORDS    .
SOURCE      Triticum sp.
  ORGANISM  Triticum sp.
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1886)
  AUTHORS   Salmeron,J.M., Weislo,L.J., Strawn,L.J., Kramer,C.M., Wang,H.X.,
            Vernooij,B.T., Levin,J.Z., Heifetz,P.B., Patton,D.A. and Que,Q.
  TITLE     Mlo-genes controlling diseases
  JOURNAL   Patent: WO 0078799-A 7 28-DEC-2000;
            Novartis AG (CH)
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BASE COUNT      405 a    564 c    531 g    386 t
ORIGIN


  Query Match             81.5%;  Score 1305.6;  DB 6;  Length 1886;
  Best Local Similarity   89.9%;  Pred. No. 3.6e-211;
  Matches 1424;  Conservative    0;  Mismatches  154;  Indels    6;  Gaps    2;

Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
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Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
Db    282 ATCATCGTCTCCGTCCTCCTGGAGCACGCGCTCCACAAGCTCGGCCATTGGTTCCACAAG 341

Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
Db    342 CGGCACAAGAACGCGCTGGCGGAGGCGCTGGAGAAGATGAAGGCGGAGCTGATGCTGGTG 401

Qy    202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261
Db    402 GGATTCATCTCGCTGCTGCTCGCCGTCACGCAGGACCC---AATCTCCGGGATATGCATC 458

Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
Db    459 TCCCAGAAGGCCGCCAGCATCATGCGCCCCTGCAAGGTGGAACCCGGTTCCGTCAAGAGC 518

Qy    322 agcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcagc 378
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Qy    379 ttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtc 438
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RESULT  10
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LOCUS       AF361933               1399 bp    mRNA    linear   PLN 26-AUG-2001
DEFINITION  Triticum aestivum seven transmembrane-spanning protein (Mlo1) mRNA,
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ACCESSION   AF361933
VERSION     AF361933.1  GI:15290590
KEYWORDS    .
SOURCE      bread wheat.
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            Pooideae; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 1399)
  AUTHORS   Devoto,A., Hartmann,A., Piffanelli,P., Elliott,C., Simmons,C.,
            Taramino,G., Goh,C.-S., Schulze-Lefert,P. and Panstruga,R.
  TITLE     Co-Evolution among intracellular domains and the C-terminus of the
            seven-transmembrane Mlo protein is suggested by a detailed
            computational analysis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1399)
  AUTHORS   Elliott,C.E. and Schulze-Lefert,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-MAR-2001) The Sainsbury Laboratory, John Innes
            Center, Colney Lane, Norwich NR4 7UH, UK
FEATURES             Location/Qualifiers
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BASE COUNT      324 a    407 c    374 g    294 t
ORIGIN


  Query Match             69.9%;  Score 1119;  DB 8;  Length 1399;
  Best Local Similarity   92.2%;  Pred. No. 1.3e-179;
  Matches 1179;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy    324 caagtacgttgactactgcccggagggcaaggtggcgctcatgtccacgggcagcttgca 383
          |||| ||    ||| | |  ||||||||||||||||||||||||||||||||||| ||||
Db     30 CAAGGACTACTACTGCGCCAAAGAGGGCAAGGTGGCGCTCATGTCCACGGGCAGCCTGCA 89

Qy    384 ccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcac 443
          |||||| ||| | |||||||||||||| || ||||||||||||||||||||||||||||||
Db     90 CCAGCTCCACATATTCATCTTCGTGCTAGCCGTCTTCCATGTCACCTACAGCGTCATCAT 149

Qy    444 catagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctc 503
          ||| |||||||||||||||| ||||||||||||||||||||||||||||||||||| ||||
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Db    150 CATGGCTCTAAGCCGTCTCAAGATGAGAACATGGAAGAAATGGGAGACAGAGACCGCCTC 209

Qy    504 cttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgtt 563
          ||||||||||||||||||||||||||||||||||| ||| |||| ||||||||||||||||||||
Db    210 CTTGGAATACCAGTTCGCAAATGATCCTGCGCGGCTCCGCTTCACGCACCAGACGTCGTT 269

Qy    564 cgtgaagcgccacctgggcctctccagcacccctggcatcagatgggtggtggcctttctt 623
          |||||||||| |||||||||||| |||||||||||| ||| ||||||||||||||||||||||||
Db    270 CGTGAAGCGGCACCTGGGCCTGTCCAGCACCCCCGGCGTCAGATGGGTGGTGGCCTTCTT 329

Qy    624 caggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttcat 683
          |||||||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||
Db    330 CAGGCAGTTCTTCAGGTCGGTCACCAAGGTGGACTACCTCACCTTGAGGGCAGGCTTCAT 389

Qy    684 caacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcgat 743
          |||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||| ||
Db    390 CAACGCGCACTTGTCGCAGAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTCCAT 449

Qy    744 ggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcct 803
          |||||||||||||||| |||||||| ||||||||||||||||||||| ||||||||||||
Db    450 GGAGGACGACTTCAAAGTCGTCGTTGGCATCAGCCTCCCGCTGTGGGCTGTGGCGATCCT 509

Qy    804 caccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatccctct 863
          |||||||||||||||| ||| | ||| | ||||| |||| |||| ||||||||||||||||
Db    510 CACCCTCTTCCTTGATATCGACGGGATCGGCACACTCACCTGGGTTTCTTTCATCCCTCT 569

Qy    864 cgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggccctgga 923
          | | ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    570 CATCATCCTCTTGTGTGTTGGAACCAAGCTAGAGATGATCATCATGGAGATGGCCCTGGA 629

Qy    924 gatccaggaccgggcgagcgtcatcaaggggggcccccgtggtcgagcccagcaacaagtt 983
          |||||||||||||| |||||||||||||||||||| ||||||||||||||||||||||||||||
Db    630 GATCCAGGACCGGTCGAGCGTCATCAAGGGGGCACCCGTGGTCGAGCCCAGCAACAAGTT 689

Qy    984 cttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttccagaa 1043
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    690 CTTCTGGTTCCACCGCCCCGACTGGGTCCTCTTCTTCATACACCTGACGCTGTTCCAGAA 749

Qy   1044 cgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaatgcta 1103
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Db    750 CGCGTTTCAGATGGCACATTTCGTGTGGACAGTGGCCACGCCCGGCTTGAAGGACTGCTT 809

Qy   1104 ccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccagttcct 1163
          ||| | | | |||||||||||||||||||||| ||| ||||||| ||||||||||||||||
Db    810 CCATATGAACATCGGGCTGAGCATCATGAAGGTCGTGCTGGGGCTGGCTCTCCAGTTCCT 869

Qy   1164 ctgcagctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaacatgaa 1223
          |||||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    870 GTGCAGCTACATCACCTTCCCCCTCTACGCGCTAGTCACACAGATGGGATCAAACATGAA 929

Qy   1224 gaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacggccaa 1283
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Db    930 GAGGTCCATCTTCGACGAGCAGACAGCCAAGGCGCTGACCAACTGGCGGAACACGGCCAA 989

Qy   1284 ggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgacgcaac 1343
          |||||||||||| ||||||||||||||||||||||||||| ||||||||||||||||||||||
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Qy   1344 accgagccgaggctcgtcgccgatgccgagccggggctcatcacccgtgcacctgcttca 1403
          ||| |||||||||| |||| |||||||| ||||||||||||||| || ||||||||||||||
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Qy   1404 caagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacccagca 1463
          |||||||||||| ||||| ||||||||||||| || ||||||||||||||  | |
Db   1110 GAAGGGCATGGGACGGTCTGACGATCCCCAGAGCGCACCGACCTCGCCAAGGACCATGGA 1169

Qy   1464 ggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaatcctaa 1523
          |||||||||||||||||||||||||||||||||||||||||||| || || ||||||||||||||
Db   1170 GGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCATCCTGTACACAGACTAAATCCTGC 1229

Qy   1524 cgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgcagattt 1583
          |||||| |||||||| | ||| || || |||||||| |||||||||||||| ||||||||
Db   1230 TGACAGGCGGAGGTCGGTCTCTTCATCAGCCCTCGATGCCGACATCCCCAGCGCAGATTT 1289

Qy   1584 ttccttcagccagggatga 1602
          ||||||||||||||||||||
Db   1290 TTCCTTCAGCCAGGGATGA 1308
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RESULT 11
A92838
LOCUS A92838 1635 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 12 from Patent WO9804586.
ACCESSION A92838
VERSION A92838.1 GI:6741374
KEYWORDS .
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1635)
AUTHORS Panstruga,R. and Bueschges,R.
TITLE POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN PLANTS
JOURNAL Patent: WO 9804586-A 12 05-FEB-1998;
INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES Location/Qualifiers
source 1. .1635
/organism="Hordeum vulgare"
/db_xref="taxon:4513"
/clone="MLO HOMOLOGUE"
BASE COUNT 315 a 496 c 520 g 304 t
ORIGIN

Query Match 58.7%; Score 940; DB 6; Length 1635;
Best Local Similarity 76.5%; Pred. No. 2.2e-149;
Matches 1272; Conservative 0; Mismatches 270; Indels 120; Gaps 5;

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Qy     18 ggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgc 77
          || |   | ||||||||| |||| |||||| |||||||||||||||| |||| |||||
Db     12 GGCGGGAGGTCGGGAGCTGTCGGACACGCCGACGTGGGCGGTGGCGGTAGTCTGCGCCGT 71

Qy     78 catggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttcca 137
          |||| | ||||| |||||| |||||| |||| ||||||||||||||||| ||||||||
Db     72 CATGATACTCGTCTCCGTCGCCATGGAGCACGCGCTCCACAAGCTCGGCCACTGGTTCCA 131

Qy    138 gcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgct 197
            | ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    132 CAAGTGGCGCAAGAAGGCCCTGGGGGAGGCGCTGGAGAAGATGAAGGCGGAGCTCATGCT 191

Qy    198 ggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatg 257
          ||||||||||||||||||||||||||||||||||||||||||||| ||    | || ||| ||| ||
Db    192 GGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGATCC---CGTCTCCAGGATCTG 248

Qy    258 catctccgaggatgccgccgacgtcatgtggccctgcaagc------gcggcaccgaggg 311
          ||||||| |||| |||| |||    |||   || |||||||       |||| |||  ||
Db    249 CATCTCCAAGGAGGCCGGCGAGAAGATGCTCCCGTGCAAGCCTTACGACGGCGCCGGCGG 308

Qy    312 ccgcaagcccagcaagta---------------------------------------- 329
            ||||   ||   |  |
Db    309 TGGCAAAGGCAAGGACAATCACCGGAGGCTTCTCTGGCTCCAAGGCGAGAGCGAGACCCA 368

Qy    330 ----------------------------cgttgactactgcccggagggcaaggtggc 359
                                       |  | || |  |    ||||||||||||||
Db    369 CCGCCGGTTCCTGGCTGCCCCGGCCGGAGTGGACGTCTGCGCCAAACAGGGCAAGGTGGC 428

Qy    360 gctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtctt 419
          ||| |||||  |||| ||| |||||| |||||| | ||||||||||||||||| |||||
Db    429 GCTGATGTCAGCGGGAAGCATGCACCAACTGCACATATTCATCTTCGTGCTCGCCGTCTT 488

Qy    420 ccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaa 479
          ||| |||  |||||||| |||||||  | ||||||||||||||||||    ||||||
Db    489 CCACGTCTTGTACAGCGTCGTCACCATGACCCTAAGCCGTCTCAAAATGAAGCAATGGAA 548
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Qy    480 gaaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggtt 539
          ||| |||||| | |||||| |||| |||| || |||||||| |||||||| | ||||
Db    549 GAAGTGGGAGTCGGAGACCGCCTCGCTGGAGTATCAGTTCGCGAATGATCCATCGCGGTG 608

Qy    540 ccggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctgg 599
          |||||||||||||||||||| |||| |||| ||| ||||||||||||||||||||||| ||
Db    609 CCGGTTCACGCACCAGACGACGTTGGTGAGGCGGCACCTGGGCCTCTCCAGCACCCCCGG 668

Qy    600 catcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggacta 659
          | |||||||||||||||||||||||||||||||||| ||| || ||||||||||||||
Db    669 CGTCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCACGTCGGTGACCAAGGTGGACTA 728

Qy    660 cctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgactt 719
          |||||||||| ||   |||||||||||||||||| | |||||   || || |||||||||
Db    729 CCTGACCTTGCGGCAGGGCTTCATCAACGCGCATCTCTCGCAGGGCAACAGGTTCGACTT 788

Qy    720 ccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcct 779
          |||||||||||||||||||| |||||||||||||||| |||||||| ||||||| ||
Db    789 CCACAAGTACATCAAGAGGTCGTTGGAGGACGACTTCAAAGTCGTCGTCCGCATCAGTCT 848

Qy    780 cccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgct 839
          | ||| |||   |||||| |||||| |||||||||||   || | ||| | ||||| ||
Db    849 CAAGCTCTGGTTCGTGGCGGTCCTCATCCTCTTCCTTGATTTCGACGGGATCGGCACTCT 908

Qy    840 catctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagat 899
          |||||||  ||   |  | |||||||||||||||||||| ||||| ||||||||||||||
Db    909 TCTCTGGATGTCCGTGGTTCCTCTCGTGATCCTCTTGTGGGTTGGGACCAAGCTGGAGAT 968

Qy    900 gatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcccc 959
          | | ||||||||||||||| ||||||||| ||||||| ||||||| ||||||| || ||
Db    969 GGTGATCATGGAGATGGCCCAGGAGATCCATGACCGGGAGAGCGTCGTCAAGGGTGCTCC 1028

Qy    960 cgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttctt 1019
          ||  |||||||||||||||||| |||||||||| |||| || ||||||||||||||| |
Db   1029 CGCCGTCGAGCCCAGCAACAAGTACTTCTGGTTCAACCGGCCTGACTGGGTCCTCTTCCT 1088

Qy   1020 catacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggc 1079
          ||| ||||| ||  | |||||||||||||||||||||| ||||| ||||||||||||||
Db   1089 CATGCACCTCACACTCTTCCAGAACGCGTTTCAGATGGCTCATTTCGTGTGGACAGTGGC 1148

Qy   1080 cacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggt 1139
          |||||||||||||||||||||||||| | | || |   ||||||||   ||||| ||
Db   1149 CACGCCCGGCTTGAAGAAATGCTACCACGAGAAAATGGCAATGAGCATCGCCAAGGTCGT 1208

Qy   1140 ggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgt 1199
          | ||||| ||||   |||| || | |||||||| || |||||||| ||||||||||||||
Db   1209 GCTGGGGGTAGCCGCCCAGATCTTGTGCAGCTACATCACCTTCCCGCTCTACGCGCTCGT 1268

Qy   1200 cacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgct 1259
          ||| |||||||| ||| ||||||||||   |||||||||||||||||| ||||||||||
Db   1269 CACGCAGATGGGCTCACACATGAAGAGAAGCATCTTCGACGAGCAGACGGCCAAGGCGCT 1328

Qy   1260 caccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgat 1319
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Db   1329 GACCAACTGGCGAAAGATGGCCAAGGAGAAGAAGAAGGCCCGAGACGCGGCCATGCTGAT 1388

Qy   1320 ggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccgggg 1379
          ||| ||||||  ||||| ||| || ||||||   ||||||||||||
Db   1389 GGCGCAGATGGGCGGCGGCGCGACGCCGAGCGTCGGCTCGTCGCCG-------------- 1434

Qy   1380 ctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgc 1439
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Db   1435 ----------GTGCACCTGCTCCACAAGGCCGGGGCGCGGTCCGACGACCCCCAGAGCGT 1484

Qy   1440 gcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgca 1499
          |||  | || || ||| || || |||| |   | | |                ||| |||
Db   1485 GCCGGCGTCCCCGAGGGCCGAGAAGGAAGGCGGCGGC--------------GTGCAGCA 1529

Qy   1500 cccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcga 1559
          |||| || ||   ||  ||||   ||| || ||||||| ||||||||| |||| |||||
Db   1530 TCCGGCGCGCAAGGTACCTCCTTGTGACGGGTGGAGGTCGGCCTCGTCGCCGGCGCTCGA 1589

Qy   1560 agccgacatccccagtgcagatttttccttcagccagggatg 1601
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Db   1590 CGCTCACATCCCCGGTGCAGATTTTGGCTTCAGCACGCAACG 1631
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RESULT 12
AF384030
LOCUS AF384030 1740 bp mRNA linear PLN 26-AUG-2001
DEFINITION Oryza sativa seven transmembrane protein MLO2 mRNA, complete cds.
ACCESSION AF384030
VERSION AF384030.1 GI:15290604
KEYWORDS .
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 1740)
AUTHORS Devoto,A., Hartmann,H.A., Piffanelli,P., Elliott,C., Simmons,C., Taramino,G., Goh,C.-S., Cohen,F.E., Schulze-Lefert,P. and Panstruga,R.
TITLE Molecular phylogeny and domain-specific co-evolution of the plant-specific seven transmembrane MLO family
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1740)
AUTHORS Elliott,C. and Schulze-Lefert,P.
TITLE Direct Submission
JOURNAL Submitted (22-MAY-2001) The Sainsbury Laboratory, Colney Lane, Norwich NR4 7UH, UK
FEATURES Location/Qualifiers
source 1. .1740
/organism="Oryza sativa"
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/db_xref="taxon:4530"
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/product="seven transmembrane protein MLO2"
/protein_id="AAK94907.1"
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KREKKAMGEALEKIKAELMLLGFISLLLTVAQTPISKICIPESAANIMLPCKAGQDIV
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VLAVFHVTYCVITMALGRLKMKKWKKWELETNSLEYQFANDPSRFRFTHQTSFVKRHL
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FKVVVGISLPLWFVAILVLFLDIQGFGTLIWISFVPLVILMLVGTKLEMVIMEMAQEI
QDRATVIKGAPVVEPSNKYFWFNRPDWVLFFIHLILFQNAFQMAHFVWTLATPGLKKC
FHENMGLSIMKVVVGIFIQFLCSYSTFPLYALVTQMGSNMKKTIFEEQTMKALMNWRK
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DMYPVPVAPVVRPHGFNRTDPDKRRAASSSAIQVDIADSDFSFSVQR"
BASE COUNT 396 a 446 c 534 g 364 t
ORIGIN

Query Match 53.9%; Score 863.8; DB 8; Length 1740;
Best Local Similarity 73.3%; Pred. No. 1.7e-136;
Matches 1220; Conservative 0; Mismatches 322; Indels 123; Gaps 4;

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Qy     24 ggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatggt 83
          || | ||| | ||||||||||||||| |||||||||||| ||||||| ||||| ||| ||
Db     73 GGGGAGGGCGTTGCCGGAGACGCCGACGTGGGCGGTGGCCGTGGTCTGCGCCGTCATCGT 132

Qy     84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
          ||||||  ||||||  ||||||  ||||||||||||||||||||||||||||||  | ||
Db    133 GCTCGTCTCCGTCGCCATGGAGCACGGCCTCCACAAGCTCGGCCATTGGTTCCATAAGCG 192

Qy    144 gcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtggg 203
          | | |||||||||| || | || ||||| |||||||| || || ||| | |||||| ||||
Db    193 GGAGAAGAAGGCCATGGGCGAAGCGCTCGAGAAGATCAAAGCAGAGTTGATGCTGCTGGG 252

Qy    204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
          ||||||||| |||||||||  ||  | ||    ||   |||| |||||||||||||| |
Db    253 CTTCATATCGCTGCTCCTCACTGTGGCACAAACGCC---CATCTCCAAGATATGCATCCC 309
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Qy    264 cgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccag 323
          |||   || ||| || |||||  ||| ||||||   ||    ||   |  ||||  |
Db    310 GGAGTCAGCTGCCAACATCATGCTGCCGTGCAAGGCAGGGCAAGATATCGTCAAGGGCCT 369

Qy    324 caag------------------------------------------------------- 327
          |||
Db    370 GAAGGGAAAAAAGGACCATCGCCGGAGGCTTCTCTGGTACACCGGAGAAGAAGAGAGCCA 429

Qy    328 ----------------------------tacgttgactactgcccggagggcaaggtggc 359
                                       | | | ||| |   |    ||||||||||||
Db    430 TCGCCGGTCACTGGCCGGCGCCGCCGGCGAGGATTACTGCGCGCAATCGGGCAAGGTGGC 489

Qy    360 gctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtctt 419
          ||| |||||  ||||| || |||||||||||||| | ||||| |||||||||||||| ||
Db    490 GCTGATGTCATCGGGCGGCATGCACCAGCTGCACATATTCATTTTCGTGCTCGCGGTGTT 549

Qy    420 ccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaa 479
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Db    550 CCACGTCACCTACTGCGTCATCACCATGGCTCTAGGGCGTCTCAAAATGAAGAAATGGAA 609

Qy    480 gaaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggtt 539
          ||| |||||   |||||||| ||| ||||| || |||||||||| |||||| |||| ||
Db    610 GAAGTGGGAATTAGAGACCAACTCGTTGGAGTATCAGTTCGCAAACGATCCTTCACGATT 669

Qy    540 ccggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctgg 599
          |||||||||||| ||||| |||||||||| || || ||||| || || ||||| |||||
Db    670 CCGGTTCACGCATCAGACATCGTTCGTGAAACGGCATCTGGGACTGTCAAGCACACCTGG 729

Qy    600 catcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggacta 659
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Db    730 GCTCAGATGGATTGTGGCGTTCTTCAGGCAGTTCTTCGGGTCTGTCACCAAGGTGGACTA 789

Qy    660 cctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgactt 719
          ||||||| || ||  |||||||||||| |||||||||||||| || ||||||||||||||
Db    790 CCTGACCATGCGGCAAGGCTTCATCAATGCGCATTTGTCGCAGAATAGCAAGTTCGACTT 849

Qy    720 ccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcct 779
          ||||||  |||||||||||||  | ||||||||  ||||| || ||||| ||||||||||
Db    850 CCACAAATACATCAAGAGGTCATTAGAGGACGATTTCAAAGTTGTCGTTGGCATCAGCCT 909

Qy    780 cccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgct 839
          |||  |||||  ||| ||||||||    |||||||||| ||| | ||| | ||||||||
Db    910 CCCATTGTGGTTTGTCGCGATCCTTGTGCTCTTCCTTGATATCCAAGGGTTCGGCACGCT 969

Qy    840 catctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagat 899
          |||||||| |||||  | || ||||| |||||| |||  ||||| || ||||||||||||
Db    970 TATCTGGATCTCTTTTGTTCCACTCGTCATCCTCATGTTGGTTGGGACAAAGCTGGAGAT 1029

Qy    900 gatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcccc 959
          | | ||||||||||||| | |||||| |||||| |||| |  || |||||||| || ||
Db   1030 GGTTATCATGGAGATGGCACAGGAGATACAGGACAGGGCAACTGTGATCAAGGGAGCACC 1089

Qy    960 cgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttctt 1019
          || || || || |||||||||| |||||||||  |||| || || |||||| | |||||
Db   1090 GGTCGTTGAACCAAGCAACAAGTACTTCTGGTTTAACCGGCCTGATTGGGTCTTGTTCTT 1149

Qy   1020 catacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggc 1079
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Db   1150 CATACACTTGATACTGTTCCAGAACGCATTTCAGATGGCACATTTCGTGTGGACTCTGGC 1209

Qy   1080 cacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggt 1139
          || || ||| |||||||||||| |||     | || ||  |||| |||||||| || ||
Db   1210 AACCCCTGGCCTGAAGAAATGCTTCCATGAAAACATGGGCTTGAGTATCATGAAAGTTGT 1269

Qy   1140 ggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgt 1199
          |||||| ||    | |||||||| |||||||| |  |||||||| |||||||| |||||
Db   1270 AGTGGGGATATTCATTCAGTTCCTATGCAGCTACAGCACCTTCCCTCTCTACGCACTCGT 1329

Qy   1200 cacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgct 1259
          ||||||||||||||||||||||| | ||||||||| |||||||||   ||||| ||
Db   1330 CACACAGATGGGATCAAACATGAAGAAGACCATCTTCGAGGAGCAGACGATGAAGGCCCT 1389

Qy   1260 caccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgat 1319
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          |  |||||| |||| ||||| | |||||||||||  |||| ||| | |||  | |  |
Db   1390 GATGAACTGGAGGAAGACGGCGAGGGAGAAGAAGAAGCTCCGGGACGCCGACGAGTTCCT 1449

Qy   1320 ggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccgggg 1379
          || ||||||| ||||||| | || |||||||| ||||||||||||
Db   1450 AGCACAGATGAGCGGCGACACGACGCCGAGCCGCGGCTCGTCGCCG-------------- 1495

Qy   1380 ctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgc 1439
                    |||||||||||| ||||||   | || | ||||||| || || | ||||||
Db   1496 ----------GTGCACCTGCTGCACAAGCAAAGGGTGAGGTCGGAAGATCCGCCGAGCGC 1545

Qy   1440 gcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgca 1499
          ||  | |||||  ||  |      ||||| ||||||||||||||||||    |||||||
Db   1546 ACCGGCATCGCCGGGGTTCGCCGGAGAGGCCAGGGACATGTACCCGGTGCCCGTGGCGCC 1605

Qy   1500 cccggtgcacagactaaatcctaac------------gacaggaggaggtccgcctcgtc 1547
            ||||||     |        ||||             || | ||||||| | || || ||
Db   1606 GGTGGTGCGGCCGCATGGGTTTAACCGGACGGACCCGGATAAGAGGAGGGCGGCGTCCTC 1665

Qy   1548 gtcggccctcgaagccgacatccccagtgcagatttttccttcag 1592
          ||||||| || |||  |||||| ||  | | |||| |||||||||
Db   1666 GTCGGCCATCCAAGTTGACATCGCCGATTCTGATTTCTCCTTCAG 1710
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RESULT  13
AF388195
LOCUS       AF388195                1894 bp    mRNA    linear   PLN 15-JUL-2001
DEFINITION  Oryza sativa Mlo (Mlo) mRNA, complete cds.
ACCESSION   AF388195
VERSION     AF388195.1  GI:14718603
KEYWORDS    .
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 1894)
  AUTHORS   Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D.,
            Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.J.
  TITLE     Isolation and characterization of Mlo homolog in rice
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1894)
  AUTHORS   Kim,M.C., Lee,S.H., Kim,J.K., Chun,H.J., Kim,J.C., Heo,W.D.,
            Chung,W.S., Choi,M.S., Park,C.Y., Yoon,H.W. and Cho,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-JUN-2001) Biochemistry, Gyeongsang National
            University, Gazwa-dong 900, Chinju 660-701, Korea
FEATURES             Location/Qualifiers
     source          1. .1894
                     /organism="Oryza sativa"
                     /cultivar="Milyang 117"
                     /db_xref="taxon:4530"
     gene            1. .1894
                     /gene="Mlo"
     CDS             142. .1806
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                     /product="Mlo"
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                     /translation="MAGGGGGRALPETPTWAVAVVCAVIVLVSVAMEHGLHKLGHWFH
                     KREKKAMGEALGKIKAELMLLGFISLLLTVAQTPISKICIPESAANIMLPCKAGQDIV
                     KGLKGKKDHRRRLLWYTGEEESHRRSLAGAAGEDYCAQSGKVALMSSGGMHQLHIFIF
                     VLAVFHVTYCVITMGLGRLKMKKWKKWESQTNSLEYQFAIDPSRFRFTHQTSFVKRHL
                     GSFSSTPGLRWIVAFFRQFFGSVTKVDYLTMRQGFINAHLSQNSKFDFHKYIKRSLED
                     DFKVVVGISLPLWFVGILVLFLDIHGLGTLIWISFVPLIIVLLVGTKLEMVIMQMAQE
                     IQDRATVIQGAPVVEPSNKYFWFNRPDWVLFFIHLTLFHNAFQMAHFVWTMATPGLKK
                     CFHENIWLSIVEVIVGISLQVLCSYITFPLYALVTQMGSNMKKTIFEEQTMKALMNWR
                     KKAMEKKKVRDADAFLAQMSVDFATPASSRSASPVHLLQDHRARLDDPPSPITVASPP
                     APEEDIYPVPAAAAFCQLLDDPPDRRWMASLSADIPDFDFSFSAQR"
BASE COUNT      438 a    493 c    558 g    405 t
ORIGIN
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Query Match             50.8%;  Score 813.4;  DB 8;  Length 1894;
Best Local Similarity   71.7%;  Pred. No. 5.5e-128;
Matches 1188;  Conservative    0;  Mismatches  361;  Indels  108;  Gaps    5;

Qy      24 ggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatggt 83
           || | ||| | ||||||||||||||| |||||||||||| ||||||| ||||| ||| ||
Db     159 GGGGAGGGCGTTGCCGGAGACGCCGACGTGGGCGGTGGCCGTGGTCTGCGCCGTCATCGT 218

Qy      84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
           |||||| ||||||  |||||| |||||||||||||||||||||||||||||||||  | ||
Db     219 GCTCGTCTCCGTCGCCATGGAGCACGGCCTCCACAAGCTCGGCCATTGGTTCCATAAGCG 278

Qy     144 gcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtggg 203
           | | |||||||||| || | || ||||| | |||||| || || ||| | |||||| ||||
Db     279 GGAGAAGAAGGCCATGGGCGAAGCGCTCGGGAAGATCAAAGCAGAGTTGATGCTGCTGGG 338

Qy     204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
           ||||||||| |||||||||| ||  | ||    ||   |||| |||||||||||||| |
Db     339 CTTCATATCGCTGCTCCTCACTGTGGCACAAACGCC---CATCTCCAAGATATGCATCCC 395

Qy     264 cgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccag 323
           |||   || ||| || |||||  ||| ||||||   ||    ||   |  ||||  |
Db     396 GGAGTCAGCTGCCAACATCATGCTGCCGTGCAAGGCAGGGCAAGATATCGTCAAGGGCCT 455

Qy     324 caag---------------------------------------------------------- 327
           |||
Db     456 GAAGGGAAAAAAGGACCATCGCCGGAGGCTTCTCTGGTACACCGGAGAAGAAGAGAGCCA 515

Qy     328 ----------------------------tacgttgactactgcccggagggcaaggtggc 359
                                       | | | ||| |   |    ||||||||||||
Db     516 TCGCCGGTCACTGGCCGGCGCCGCCGGCGAGGATTACTGCGCGCAATCGGGCAAGGTGGC 575

Qy     360 gctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtctt 419
           ||| |||||  ||||| || |||||||||||||| | ||||| |||||||||||||| ||
Db     576 GCTGATGTCATCGGGCGGCATGCACCAGCTGCACATATTCATTTTCGTGCTCGCGGTGTT 635

Qy     420 ccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaa 479
           ||| |||||||| |||||||||||| | | || | || ||||||||||  | |||||||
Db     636 CCACGTCACCTACTGCGTCATCACCATGGGTTTAGGGCGCCTCAAAATGAAGAAATGGAA 695

Qy     480 gaaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggtt 539
           ||| |||||| || |||||| ||| ||||| || ||||||||||  |||||| |||| ||
Db     696 GAAGTGGGAGTCACAGACCAACTCATTGGAGTATCAGTTCGCAATCGATCCTTCACGATT 755

Qy     540 ccggttcacgcaccagacgtcgttcgtgaagcgccacctggg---cctctccagcacccc 596
           | |||||||||| |||||||||||||||||||| || |||||     |||| ||||||||
Db     756 CAGGTTCACGCATCAGACGTCGTTCGTGAAGCGGCATCTGGGATCATTCTCAAGCACCCC 815

Qy     597 tggcatcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtgga 656
           |||  |||||||| | || || |||||||||||||||  |||| ||||||||||||||
Db     816 TGGGCTCAGATGGATCGTAGCATTCTTCAGGCAGTTCTTTGGGTCCGTCACCAAGGTGGA 875

Qy     657 ctacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcga 716
           |||||||||| || ||  |||||||||||| |||||||||||||| || ||||||||||
Db     876 CTACCTGACCATGCGGCAAGGCTTCATCAATGCGCATTTGTCGCAGAATAGCAAGTTCGA 935

Qy     717 cttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcag 776
           ||||||||| ||||||||||||||  |||||||||||||||| || ||||| ||||||||
Db     936 CTTCCACAAATACATCAAGAGGTCTTTGGAGGACGACTTCAAAGTTGTCGTTGGCATCAG 995

Qy     777 cctcccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcac 836
           |||||| |||||||   || |  |||||    |||||||| || ||| | ||  |||||||
Db     996 CCTCCCTCTGTGGTTCGTCGGAATCCTTGTACTCTTCCTCGATATCCACGGTCTTGGCAC 1055

Qy     837 gctcatctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctgga 896
           || || ||||| |||||  | |||||| | ||| ||||||  ||||| |||||||| ||
Db    1056 ACTTATTTGGATCTCTTTTGTTCCTCTCATCATCGTCTTGTTAGTTGGGACCAAGCTAGA 1115

Qy     897 gatgatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggc 956
           |||| | |||||| |||||||||  ||||| |||||| |||| |  || ||| |||| ||
Db    1116 GATGGTGATCATGCAGATGGCCCAAGAGATACAGGACAGGGCCACTGTGATCCAGGGAGC 1175

Qy     957 ccccgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctctt 1016
           || ||||| || || |||||||||| |||||||||| ||||||| ||||||||| | ||
Db    1176 ACCTGTGGTTGAACCAAGCAACAAGTACTTCTGGTTCAACCGCCCTGACTGGGTCTTGTT 1235

Qy    1017 cttcatacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagt 1076
           ||||||||||||||  | ||||| |||| |||||||||||||||||| || |||||  |
Db    1236 CTTCATACACCTGACACTCTTCCATAACGCATTTCAGATGGCGCATTTCGTATGGACTAT 1295

Qy    1077 ggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggt 1136
           ||| || || ||  |||||||||||| |||     | ||  |||||||||| || | ||
Db    1296 GGCAACACCTGGTCTGAAGAAATGCTTCCATGAAAATATTTGGCTGAGCATCGTGGAAGT 1355

Qy    1137 ggtggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgct 1196
             | |||||| |  |||| ||| | || |||||||| || |||||||| ||||||||||
Db    1356 CATTGTGGGGATCTCTCTTCAGGTGCTATGCAGCTACATCACCTTCCCGCTCTACGCGCT 1415

Qy    1197 cgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggc 1256
           |||||||||||||||||  ||||||||||  | | ||||||||  ||||| |||   |||||
Db    1416 CGTCACACAGATGGGATCGAACATGAAGAAGACAATCTTCGAGGAGCAAACGATGAAGGC 1475

Qy    1257 gctcaccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgct 1316
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Db    1476 GCTGATGAACTGGAGGAAGAAGGCGATGGAGAAGAAGAAGGTCCGGGACGCGGACGCGTT 1535

Qy    1317 gatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccg 1376
             |||| ||||||| || ||||                | || |||||  | |||||||
Db    1536 CCTGGCGCAGATGAGCGTCGAC---------------TTCGCGACGCCGGCGTCGAGCCG 1580

Qy    1377 gggctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagag 1436
           |  | | || || |||||||||| ||  |   || || | ||| |||||||| | |||
Db    1581 GTCCGCGTCGCCGGTGCACCTGCTGCAGGATCACAGGGCGAGGTTGGACGACCCGCCGAG 1640

Qy    1437 cgcgcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggc 1496
           | |   |||   | |     | | |     ||    |||||| ||||||||   || |||
Db    1641 CCCAATCACGGTGGCCTCACCACCGGCACCGGAGGAGGACATATACCCGGTGCCGGCGGC 1700

Qy    1497 gcacccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccct 1556
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Db    1701 GGCTGCGTTTTGCCAGCT---GCTAGACGACCCGCCGGACAGGAGGTGGATGGCATCCTT 1757

Qy    1557 cgaagccgacatccccagtgcagatttttccttcagc 1593
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Db    1758 GTCGGCCGACATTCCCGATTTTGATTTTTCCTTCAGC 1794
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RESULT  14
AY029312
LOCUS       AY029312               1872 bp    mRNA    linear   PLN 15-JUN-2001
DEFINITION  Zea mays seven transmembrane protein Mlol mRNA, complete cds.
ACCESSION   AY029312
VERSION     AY029312.1  GI:13784974
KEYWORDS    .
SOURCE      Zea mays.
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 1872)
  AUTHORS   Briggs,S.P. and Simmons,C.R.
  TITLE     Manipulation of mlo genes to enhance disease resistance in plants
  JOURNAL   Patent: PCT WO/00/01722-B 07-JUL-1999;
REFERENCE   2  (bases 1 to 1872)
  AUTHORS   Cahoon,R.E., Miao,G.-H., Rafalski,J.A. and Taramino,G.
  TITLE     Zea mays cDNA encoding southern corn leaf blight resistance protein
  JOURNAL   Patent: PCT WO9923235-B 05-NOV-1999;
REFERENCE   3  (bases 1 to 1872)
  AUTHORS   Devoto,A., Hartmann,A., Piffanelli,P., Elliott,C., Simmons,C.R.,
            Taramino,G., Goh,C.-S., Cohen,F.E., Schulze-Lefert,P. and
            Panstruga,R.
  TITLE     Molecular phylogeny and domain-specific co-evolution of the
            plant-specific seven transmembrane Mlo family
  JOURNAL   Unpublished
REFERENCE   4  (bases 1 to 1872)
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  AUTHORS   Simmons,C.R., Taramino,G. and Powell,W.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-APR-2001) Bioinformatics Department, Pioneer, A
            DuPont Company, 7250 N.W. 62nd Avenue, Emerson, Box 552, Johnston,
            IA 50131, USA
FEATURES             Location/Qualifiers
     source          1. .1872
                     /organism="Zea mays"
                     /cultivar="B73"
                     /db_xref="taxon:4577"
                     /chromosome="1"
                     /map="bin1"
                     /note="common: maize"
     CDS             17. .1708
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                     /codon_start=1
                     /product="seven transmembrane protein Mlo1"
                     /protein_id="AAK38337.1"
                     /db_xref="GI:13784975"
                     /translation="MAGGGGRDLPSTPTWAVALVCAVIVLVSVAMEHGLHKLGHWFH
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                     QLHIFIFVLAVFHIVYSVATMALGRLKMRKWKKWESETNSLEYQYANDPSRFRFTHQT
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                     KRSLEDDFKVVVGISLPLWFVAIFTLLIDIKGFGTLVWISFVPLVILLLVGAKLEVVI
                     MEMAKEIQDKATVIKGAPVVEPSDRFFWFNRPGWVLFLIHLTALPERLPDGAFRLDTA
                     HPRPEEMLPREAGLSIMKVAVGLVLQVLCSYITFPLYALVTQMGSHMKKTIFEEQTAK
                     AVMKWRKTAKDKVRQREAAGFLDVLTSADTTPSHSRATSPSRGNSPVHLLHKYRGRSE
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BASE COUNT      394 a    560 c    554 g    364 t
ORIGIN
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  Best Local Similarity  71.8%;  Pred. No. 8.2e-128;
  Matches 1218;  Conservative    0;  Mismatches  356;  Indels  122;  Gaps    7;

Qy      16 ggggtgccggcgcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgcc 75
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Db      26 GGCGGGGGCGGCCGGGACCTGCCGTCGACGCCGACGTGGGCGGTGGCCCTGGTGTCGCCC 85

Qy      76 gccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttc 135
           | ||| ||||||||| ||||||  ||||||  || ||||||||||||||||||||| ||||||
Db      86 GTCATCGTGCTCGTCTCCGTCGCCATGGAGCATGGCCTCCACAAGCTCGGCCACTGGTTC 145

Qy     136 cagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatg 195
           ||    ||||| |||||||||  || |||||||  ||||||||||  || ||  ||| | |||
Db     146 CATACGCGGCAGAAGAAGGCCATGCGGGAGGCCCTGGAGAAGATCAAAGCAGAGTTGATG 205

Qy     196 ctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagata 255
           ||| ||||||||||| || |||||||||  |||   ||||   ||   |||| ||||||||
Db     206 CTGATGGGCTTCATCTCGCTGCTCCTCGCCGTGGGGCAGACGCC---CATCTCCAAGATA 262

Qy     256 tgcatctccgaggatgccgccgacgtcatgtggccctgcaag---------------------- 297
           |||||| | |   | || | |  | |||||  ||| ||||||
Db     263 TGCATCCCGGCCAAGGCTGGCAGCATCATGCTGCCGTGCAAGCCGCCGAAAGGCGCCGCC 322

Qy     298 ------------------------------------------------------------ 297

Db     323 GCCGCCGCCGACGACGACAAGAGCGACGGCCGCCGGAGACTCCTCTGGTACCCGCCGTAC 382

Qy     298 ---------------------------cgcggcaccgagggccgcaagcccagcaagtac 330
                                        ||| |   |  | | ||  | |    |  ||
Db     383 CCTGGATACGATGAGCCCGGGCACCACCGCCGTTTCCTCGCCGGCGCGGCTCCGGACGAC 442

Qy     331 gttgactactgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctg 390
           |||  | |     | |||||||| | ||||| ||| ||| | || | |||||||||
Db     443 AACTACTGCAGTGACCAAGGCAAGGTGTCCCTCATCTCCTCGGCCGGCGTCCACCAGCTG 502

Qy     391 cacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagct 450
           ||| ||||||||||||||||||||| |||||| ||  ||||||||||  |||||| ||
Db     503 CACATCTTCATCTTCGTGCTCGCGGTGTTCCATATCGTCTACAGCGTCGCCACCATGGCG 562

Qy     451 ctaagccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctccttggaa 510
           ||  | |||||||||||||| | ||||||||||||||  | |||||| |||| |||||
Db     563 CTGGGGCGTCTCAAAATGAGGAAATGGAAGAAATGGGAATCGGAGACCAACTCCCTGGAA 622

Qy     511 taccagttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtgaag 570
           ||||||| |||||| || ||| ||||||||||||||||||||||||||||||||||||||
Db     623 TACCAGTACGCAAACGACCCTTCACGGTTCCGGTTCACGCACCAGACGTCGTTCGTGAAG 682

Qy     571 cgccacctgggcctctccagcacccctggcatcagatgggtggtggccttcttcaggcag 630
           || ||||||||||||| ||||||||||  | |||||||| |||| ||||||||||||
Db     683 CGGCACCTGGGCCTCTCGAGCACCCCTGGAGTGAGATGGGTCGTGGCGTTCTTCAGGCAG 742

Qy     631 ttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcg 690
           ||||||  ||| || |||||||||||| |||||||| || ||   || |||||||||
Db     743 TTCTTCGCGTCCGTGACCAAGGTGGATTACCTGACCATGCGGCAGGGGTTCATCAACTAC 802

Qy     691 catttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcgatggaggac 750
           ||| ||||||  | || |||||||| |||||||  |||||||||||| |||| ||||||||
Db     803 CATCTGTCGCCCAGCACCAAGTTCAACTTCCAGCAGTACATCAAGCGGTCCTTGGAGGAC 862

Qy     751 gacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctc 810
           |||||||| |||||||| |||||||| ||||||||||||    || || ||| |||| |||
Db     863 GACTTCAAAGTCGTCGTTGGCATCAGTCTCCCGCTGTGGTTCGTCGCCATCTTCACTCTC 922

Qy     811 ttccttgacatcaatggggttggcacgctcatctggatttctttcatccctctcgtgatc 870
           ||  | || ||||| ||  | ||||||||  |||||||  |||||  |||| |||| ||
Db     923 TTGATCGATATCAAGGGATTCGGCACGCTTGTCTGGATCTCTTTTGTCCCGCTCGTTATA 982

Qy     871 ctcttgtgtgttggaaccaagctggagatgatcatcatggagatggccctggagatccag 930
           ||| ||   |||||  |||||||||||| |  ||||||||||||||||  ||||||  |||
Db     983 CTCCTGCTAGTTGGGGCCAAGCTGGAGGTTGTCATCATGGAGATGGCCAAGGAGATACAG 1042

Qy     931 gaccgggcgagcgtcatcaagggggcccccgtggtcgagcccagcaacaagttcttctgg 990
           |||  |||||  |||||||||||||| || ||||| ||||| ||  ||| ||||||||||
Db    1043 GACAAGGCGACGGTCATCAAGGGGGCGCCTGTGGTGGAGCCAAGTGACAGGTTCTTCTGG 1102

Qy     991 ttccaccgccccgactgggtcctcttcttcatacacctgac-gttgttccagaacgcgtt 1049
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Db    1103 TTTAACCGCCCTGGCTGGGTCCTCTTCCTCATCCACCTCACGGCTCTTCCAGAACGCCTT 1162

Qy     1050 tcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaatgctaccacac 1109
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Db     1163 CCAGATGGCGCATTTCGTTTGGACACTGCTCACCCCAGACCTGAAGAAATGCTACCACGA 1222

Qy     1110 gcagatcgggctgagcatcatgaaggtggtggtggggctagctctccagttcctctgcag 1169
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Db     1223 G-AGGCTGGGCTTAGCATCATGAAGGTTGCGGTGGGGCTGGTTCTCCAGGTCCTCTGCAG 1281

Qy     1170 ctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtc 1229
            || || |||||||| |||||||||||||||| |||||||| ||  |||||||| | |
Db     1282 TTACATCACCTTCCCGCTCTACGCGCTCGTCACGCAGATGGGGTCGCACATGAAGAAGAC 1341

Qy     1230 catcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacggccaaggagaa 1289
            ||||||||| ||||||||| |||||||| | |  || ||||| || ||||||||||| ||
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Db     1402 GGTGCGGCAGCGGGAGGCGGCAGGCTTCCTCGACGTGCTGACGAGCGCCGACACCACGCC 1461

Qy     1347 gagccgaggctcgtcgccgatgccgagccgggggctcatcacccgtgcacctgcttcacaa 1406
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Qy     1407 gggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacccagcagga 1466
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Db     1522 GTACAGGGGCAGGTCGGAGGAACCGCAGAGCGGGCCGGCGTCGCCGGG------GCGGGA 1575

Qy     1467 ggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaatcctaacga 1526
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Db     1576 GCTCGGGGACATGTACCCGGTGGCTGACCAGCATCGCCTGCACAGGCTGGACCC---CGA 1632

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Qy   1587 cttcagccagggatga 1602
Db   1693 TTTTAGCATGCGGTGA 1708


RESULT  15
A92837
LOCUS       A92837                 1611 bp    DNA     linear   PAT 22-JAN-2000
DEFINITION  Sequence 11 from Patent WO9804586.
ACCESSION   A92837
VERSION     A92837.1  GI:6741373
KEYWORDS    .
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 1611)
  AUTHORS   Panstruga,R. and Bueschges,R.
  TITLE     POLYNUCLEOTIDE AND ITS USE FOR MODULATING A DEFENCE RESPONSE IN
            PLANTS
  JOURNAL   Patent: WO 9804586-A 11 05-FEB-1998;
            INNES JOHN CENTRE INNOV LTD (GB); PANSTRUGA RALPH (GB)
FEATURES             Location/Qualifiers
     source          1. .1611
                     /organism="Oryza sativa"
                     /db_xref="taxon:4530"
                     /clone="MLO HOMOLOGUE"
BASE COUNT      348 a    451 c    450 g    362 t
ORIGIN


  Query Match             47.9%;  Score 767.2;  DB 6;  Length 1611;
  Best Local Similarity   71.6%;  Pred. No. 3.6e-120;
  Matches 1152;  Conservative    0;  Mismatches  383;  Indels   75;  Gaps    8;

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Db      23 CGCGGGAGTTGCCGGAGACGCCGACGTGGGCGGTGGCCGTCGTCTGCGCCGTCCTCGTGC 82

Qy      86 tcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccggc 145
Db      83 TCGTCTCCGCCGCCATGGAGCACGGCCTCCACAACCTCAGCCA-----TAAAACCACCGC 137

Qy     146 acaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtgggct 205
Db     138 AGAAGTTCTCATATTTCTTGTCCTATCTGCACTT----GCAGAGCTGATGCTGCTGGGCT 193

Qy     206 tcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctccg 265
Db     194 TCATATCCCTGCTTCTCACCGTGGCACAGGCGCC---CATCTCCAAGATCTGCATCCCCA 250

Qy     266 aggatgccgccgacgtcatgtggccctgcaag---------------------------- 297
Db     251 AGTCGGCTGCCAACATCTTGTTGCCGTGCAAGGCAGGCCAAGATGCCATCGAAGAAGAAG 310

Qy     298 ----------cgcggcaccgagggccgcaagcccagcaagtacgttgactactgcccgg 346
Db     311 CAGCAAGTGGTCGCCGGTCCTTGGCCGGCGCCGGCGGCGGGGACTACTGCTCGAAATTCG 370

Qy     347 agggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcg 406
Db     371 ATGGCAAGGTGGCGCTGATGTCGGCAAAGAGCATGCACCAGCTGCACATTTTCATCTTCG 430

Qy     407 tgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaa 466
Db     431 TGCTCGCCGTGTTCCATGTTACCTACTGCATCATCACCATGGGTTTAGGGCGCCTCAAAA 490

Qy     467 tgagaacatggaagaaatgggagacagagaccacctccttggaataccagttcgcaaatg 526
Db     491 TGAAGAAATGGAAGAAGTGGGAGTCACAGACCAACTCATTGGAGTATCAGTTCGCAATCG 550

Qy     527 atcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcgccacctggg---cc 583
Db     551 ATCCTTCACGATTCAGGTTCACGCATCAGACGTCGTTCGTGAAGCGGCATCTGGGATCAT 610

Qy     584 tctccagcacccctggcatcagatgggtggtggccttcttcaggcagttcttcaggtcag 643
Db     611 TCTCAAGCACCCCTGGGCTCAGATGGATCGTAGCATTCTTCAGGCAGTTCTTTGGGTCCG 670

Qy     644 tcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaa 703
Db     671 TCACCAAGGTGGACTACCTGACCATGCGGCAAGGCTTCATCAATGCGCATTTGTCGCAGA 730

Qy     704 acagcaagttcgacttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcg 763
Db     731 ATAGCAAGTTCGACTTCCACAAATACATCAAGAGGTCTTTGGAGGACGACTTCAAAGTTG 790

Qy     764 tcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatca 823
Db     791 TCGTTGGCATCAGCCTCCCTCTGTGGTTCGTCGGAATCCTTGTACTCTTCCTCGATATCC 850

Qy     824 atggggttggcacgctcatctggatttctttcatccctctcgtgatcctcttgtgtgttg 883
Db     851 ACGGTCTTGGCACACTTATTTGGATCTCTTTTGTTCCTCTCATCATCGTCTTGTTAGTTG 910

Qy     884 gaaccaagctggagatgatcatcatggagatggccctggagatccaggaccgggcgagcg 943
Db     911 GGACCAAGCTAGAGATGGTGATCATGGAGATGGCCCAAGAGATACAGGACAGGGCCACTG 970

Qy     944 tcatcaaggggggcccccgtggtcgagcccagcaacaagttcttctggttccaccgccccg 1003
Db     971 TGATCCAGGGAGCACCTATGGTTGAACCAAGCAACAAGTACTTCTGGTTCAACCGCCCTG 1030

Qy    1004 actgggtcctcttcttcatacacctgacgttgttccagaacgcgtttcagatggcgcatt 1063
Db    1031 ACTGGGTCTTGTTCTTCATACACCTGACACTCTTCCATAACGCATTTCAGATGGCGCATT 1090

Qy    1064 ttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctga 1123
Db    1091 TCGTATGGACTATGGCAACACCTGGTCTGAAGAAATGCTTCCATGAAAATATTTGGCTGA 1150

Qy    1124 gcatcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgaccttcc 1183
Db    1151 GCATCGTGGAAGTCATTGTGGGGATCTCTCTTCAGGTGCTATGCAGCTACATCACCTTCC 1210

Qy    1184 ccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagc 1243
Db    1211 CGCTCTACGCGCTCGTCACACAGATGGGATCGAACATGAAGAAGACAATTTTCGAGGAGC 1270

Qy    1244 agacgtccaaggcgctcaccaactggcggaacacggccaaggagaagaagaaagtccgag 1303
Db    1271 AAACGATGAAGGCGCTGATGAACTGGAGGAAGAAGGCGATGGAGAAGAAGAAGGTCCGGG 1330

Qy    1304 acacggacatgctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgc 1363
Db    1331 ACGCCGACGCGTTCCTGGCGCAGATGAGCGTCGAC----------TTCGCGACGC 1375

Qy    1364 cgatgccgagccgggggctcatcacccgtgcacctgcttcacaagggcatggggcggtcgg 1423
Db    1376 CGGCGTCGAGCCGGTCCGCGTCGCCGGTGCACCTGCTGC---AGGTCACAGGGCGGGTCG 1432

Qy    1424 acgacccccagagcgcgcccacctcgccaaggacccagcaggaggctagggacatgtacc 1483
Db    1433 GACGCCCGCCGAGCCCAATCACGGTGGCCTCACCACCGGCACCGGAGGAGGACATGTACC 1492

Qy    1484 cggttgtggtggcgcacccggtgcacagactaaatcctaacgacaggaggaggtccgcct 1543
Db    1493 CGGTGCCGGCGGCGGCTGCGTCTCGCCAGCT---GCTAGACGACCCGCCGGACAGGAGGT 1549

Qy    1544 cgtcgtcggccctcgaagccgacatccccagtgcagatttttccttcagc 1593
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Search completed: July 23, 2002, 09:37:03
Job time: 2196 sec

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 23, 2002, 14:24:40 ; Search time 69 Seconds
(without alignments)
1336.323 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSSALEADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2434	87.3	534	10	Q94F72	Q94f72 triticum ae
2	2429	87.1	534	10	Q94FR4	Q94fr4 triticum ae
3	2411	86.5	534	10	Q94F71	Q94f71 triticum ae
4	2084	74.7	435	10	Q94FR3	Q94fr3 triticum ae
5	2049.5	73.5	555	10	Q9SNK5	Q9snk5 oryza sativ
6	2046.5	73.4	555	10	Q93XC8	Q93xc8 oryza sativ
7	1880	67.4	554	10	Q94EX3	Q94ex3 oryza sativ
8	1727	61.9	563	10	Q94CH4	Q94ch4 zea mays (m
9	1257	45.1	515	10	Q94CG9	Q94cg9 zea mays (m
10	1255.5	45.0	576	10	Q94KB3	Q94kb3 arabidopsis
11	1253.5	45.0	573	10	Q9SXB6	Q9sxb6 arabidopsis
12	1234.5	44.3	583	10	Q9SY94	Q9sy94 arabidopsis
13	1221.5	43.8	583	10	Q94KB7	Q94kb7 arabidopsis
14	1192	42.8	580	10	Q9FRJ3	Q9frj3 oryza sativ
15	1160	41.6	565	10	Q94CH3	Q94ch3 zea mays (m
16	1134.5	40.7	569	10	Q9FKY5	Q9fky5 arabidopsis
17	1132.5	40.6	593	10	Q94KB5	Q94kb5 arabidopsis
18	1088.5	39.0	467	10	Q9C8E5	Q9c8e5 arabidopsis
19	1088	39.0	574	10	Q9SHM0	Q9shm0 arabidopsis
20	1049	37.6	443	10	Q9C855	Q9c855 arabidopsis
21	961	34.5	508	10	Q94KB9	Q94kb9 arabidopsis
22	901	32.3	339	10	Q94KB4	Q94kb4 arabidopsis
23	888.5	31.9	406	10	Q94KB6	Q94kb6 arabidopsis
24	888.5	31.9	492	10	Q94CG7	Q94cg7 zea mays (m
25	888	31.9	478	10	Q94KB2	Q94kb2 arabidopsis
26	881	31.6	171	10	Q94G68	Q94g68 triticum ae
27	853.5	30.6	429	10	Q9STW9	Q9stw9 arabidopsis
28	804.5	28.9	554	10	Q94KB1	Q94kb1 arabidopsis
29	801.5	28.7	496	10	Q94CH2	Q94ch2 zea mays (m
30	790.5	28.4	485	10	Q9M3E8	Q9m3e8 arabidopsis
31	790	28.3	573	10	Q9FI00	Q9fi00 arabidopsis
32	783.5	28.1	499	10	Q94CG8	Q94cg8 zea mays (m
33	735.5	26.4	509	10	Q94CH1	Q94ch1 zea mays (m
34	712.5	25.6	573	10	Q94KB8	Q94kb8 arabidopsis
35	631	22.6	507	10	Q9LQY2	Q9lqy2 arabidopsis
36	614.5	22.0	311	10	Q940N5	Q940n5 arabidopsis
37	600.5	21.5	469	10	Q94CG6	Q94cg6 zea mays (m
38	274	9.8	103	10	Q9XJ52	Q9xj52 triticum ae
39	243	8.7	149	10	Q94CH0	Q94ch0 zea mays (m
40	114	4.1	628	16	Q92F14	Q92f14 listeria in
41	108.5	3.9	389	4	Q9H6I8	Q9h6i8 homo sapien
42	107	3.8	1826	3	Q9P377	Q9p377 schizosacch
43	105	3.8	920	4	Q96PH5	Q96ph5 homo sapien
44	103.5	3.7	770	17	Q97U12	Q97u12 sulfolobus
45	103	3.7	712	10	Q94EK6	Q94ek6 pisum sativ

ALIGNMENTS

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ID Q94F72 PRELIMINARY; PRT; 534 AA.
AC Q94F72;
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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MLO PROTEIN.
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE FROM N.A.
RA Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
RT "Cloning, location and expression of MLo gene from wheat.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF384144; AAK60566.1; -.
SQ SEQUENCE 534 AA; 60298 MW; 6C9640F30FDE5189 CRC64;

Query Match 87.3%; Score 2434; DB 10; Length 534;
Best Local Similarity 88.8%; Pred. No. 3.2e-225;
Matches 469; Conservative 22; Mismatches 33; Indels 4; Gaps 3;

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Db       9 PARTLPETPSWAVALVFAVMIIVSVLLEHALHKLGHWFHKRHKNALAEALEKMKAELMLV 68

Qy      68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
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Db      69 GFISLLLAVTQDP-ISGICISQKAASIMRPCK-VEPGSVKSKYKDYYCAKEGKVALMSTG 126

Qy     126 SLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
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Db    247 RSMEDDFKVVVGISLPLWAVAILTLFLDIDGIGTLTWVSFIPLIILLCVGTKLEMIIMEM 306

Qy    306 ALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 365

Db    307 ALEIQDRSSVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 366

Qy    366 KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN 425

Db    367 DCFHMNIGLSIMKVVLGLALQFLCSYITFPLYALVTQMGSNMKRSIFDEQTAKALTNWRN 426

Qy    426 TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485

Db    427 TAKEKKKVRDTDMLMAQMIGDATPSRGTSPMPSRGSSPVHLLQKGMGRSDDPQSAPTSPR 486

Qy    486 TQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533

Db    487 TMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDADIPSADFSFSQG 534


RESULT   2
Q94FR4
ID   Q94FR4      PRELIMINARY;      PRT;   534 AA.
AC   Q94FR4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SEVEN TRANSMEMBRANE-SPANNING PROTEIN.
GN   MLO2.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. BOB WHITE;
RA   Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.;
RT   "Co-Evolution among intracellular domains and the C-terminus of the
RT   seven-transmembrane Mlo protein is suggested by a detailed
RT   computational analysis.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF361932; AAK94904.1; -.
KW   Transmembrane.
SQ   SEQUENCE   534 AA;  60427 MW;  2DB2384078336D00 CRC64;


  Query Match             87.1%;  Score 2429;  DB 10;  Length 534;
  Best Local Similarity   88.0%;  Pred. No. 9.6e-225;
  Matches  469;  Conservative   22;  Mismatches   38;  Indels    4;  Gaps    3;

Qy      3 DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62

Db      4 DDEYPPARTLPETPSWAVALVFAVMIIVSVLLEHALHKLGHWFHKRHKNALAEALEKIKA 63

Qy     63 ELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVA 120

Db     64 ELMLVGFISLLLAVTQDP-ISGICIPEKAASIMRPCKL-PPGSVKSKYKDYYCAKQGKVS 121

Qy    121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180

Db    122 LMSTGSLHQLHIFIFVLAVFHVTYSVIIMALSRLKMRTWKKWETETASLEYQFANDPARF 181

Qy    181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240

Db    182 RFTHQTSFVKRHLGLSSTPGVRWVVAFFRQFFRSVTKVDYFTLRAGFINAHLSHNSKFDF 241

Qy    241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300

Db    242 HKYIKRSMEDDFKVVVGISLPLWCVAILTLFLDIDGIGTLTWISFIPLVILLCVGTKLEM 301

Qy    301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360

Db    302 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 361

Qy    361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420

Db    362 TPGLKKCFHMHIGLSIMKVVLGLALQFLCSYITFPLYALVTQMGSNMKRSIFDEQTAKAL 421

Qy    421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480

Db    422 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGASPMPSRGSSPVHLLHKGMGRSDDPQST 481

Qy    481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533

Db    482 PTSPRAMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDVDIPSADFSFSQG 534


RESULT   3
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ID   Q94F71      PRELIMINARY;      PRT;   534 AA.
AC   Q94F71;
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DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MLO1 PROTEIN.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Yu L., Niu J.-S., Ma Z.-Q., Chen P.-D., Liu D.-J.;
RT   "Cloning, characterization analysis and expression of MLo1 gene from
RT   wheat.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF384145; AAK60567.1; -.
SQ   SEQUENCE   534 AA;  60402 MW;  7CB1B6B64F3C5E66 CRC64;


  Query Match             86.5%;  Score 2411;  DB 10;  Length 534;
  Best Local Similarity   87.6%;  Pred. No. 5.2e-223;
  Matches  467;  Conservative   22;  Mismatches   40;  Indels    4;  Gaps    3;

Qy      3 DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62

Db      4 DDEYPPARTLPETPSWAVALVFAVMIIVSVLLEHALHKLGHWFHKRHKNALAEALEKIKA 63

Qy     63 ELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVA 120

Db     64 ELMLVGFISLLLAVTQDP-ISGICIPEKAASIMRPCKL-PPGSVKSKYKDYYCAKQGKVS 121

Qy    121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180

Db    122 LMSTGSLHQLHIFIFVLAVFHVTYSVIIMALSRLKMRTWKKWETETASLEYQFANDPARF 181

Qy    181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240

Db    182 RFTHQTSFVKRHLGLSSTPGVRWVVASFRQFFRSVTKVDYLTLRAGFINAHLSHNSKFDF 241

Qy    241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300

Db    242 HKYIKRSMEDDFKVVVGISLPLWCVAILTLFLDIDGIGTLTWISFIPLVILLCVGTKLEM 301

Qy    301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360

Db    302 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 361

Qy    361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
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Db    362 TRGLKKCFHMHIGLSIMKVVLGLALQFLCSYITFPLYALVTQMGSNMKRSIFDEQTAKAL 421

Qy    421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
          ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db    422 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGASPMPSRGSSPVHLLHKGMGRSDDPQST 481

Qy    481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
          |||||  :|||||||||||||||||| ||||| |||||: ||||||||||||
Db    482 PTSPRAMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDVDIPSADFSFSQG 534


RESULT   4
Q94FR3
ID   Q94FR3      PRELIMINARY;      PRT;   435 AA.
AC   Q94FR3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SEVEN TRANSMEMBRANE-SPANNING PROTEIN (FRAGMENT).
GN   MLO1.
OS   Triticum aestivum (Wheat).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Triticum.
OX   NCBI_TaxID=4565;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. BOB WHITE;
RA   Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C.-S., Schulze-Lefert P., Panstruga R.;
RT   "Co-Evolution among intracellular domains and the C-terminus of the
RT   seven-transmembrane Mlo protein is suggested by a detailed
RT   computational analysis.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF361933; AAK94905.1; -.
KW   Transmembrane.
FT   NON_TER       1      1
SQ   SEQUENCE   435 AA;  49354 MW;  3D96BD52FA62D42B CRC64;


  Query Match             74.7%;  Score 2084;  DB 10;  Length 435;
  Best Local Similarity   91.9%;  Pred. No. 1.1e-191;
  Matches  397;  Conservative   15;  Mismatches   18;  Indels    2;  Gaps    1;

Qy    104 GRKPSKYVDY--CPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKK 161
          |   ||| ||    ||||||||||||||||:||||||||||||||| :||||||||||||
Db      4 GSVKSKYKDYYCAKEGKVALMSTGSLHQLHIFIFVLAVFHVTYSVIIMALSRLKMRTWKK 63

Qy    162 WETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYL 221
          ||||| |||||||||||| ||||||||||||||||||:||||||||||||||||||||||
Db     64 WETETASLEYQFANDPARLRFTHQTSFVKRHLGLSSTPGVRWVVAFFRQFFRSVTKVDYL 123

Qy    222 TLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLI 281
          ||||||||||||||||||||||||||||||||||||||||| ||||||||||:|:|||
Db    124 TLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWAVAILTLFLDIDGIGTLT 183

Qy    282 WISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFI 341
          |:||||:|||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db    184 WVSFIPLIILLCVGTKLEMIIMEMALEIQDRSSVIKGAPVVEPSNKFFWFHRPDWVLFFI 243

Qy    342 HLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVT 401
          |||||||||||||||||||| |:|  |||||||||:|||||||||:|||||||||||||||
Db    244 HLTLFQNAFQMAHFVWTVATPGLKDCFHMNIGLSIMKVVLGLALQFLCSYITFPLYALVT 303

Qy    402 QMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGS 461
          |||||||||||||:|||||||||||||||||||||||||||||||||:||||||||
Db    304 QMGSNMKRSIFDEQTAKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGTSPMPSRGS 363

Qy    462 SPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEA 521
          |||||| |||||||||||||||| :|||||||||||||||||| ||||| |||||:|
Db    364 SPVHLLQKGMGRSDDPQSAPTSPRTMEEARDMYPVVVAHPVHRLNPADRRRSVSSSALDA 423

Qy    522 DIPSADFSFSQG 533
          ||||||||||||
Db    424 DIPSADFSFSQG 435


RESULT   5
Q9SNK5
ID   Q9SNK5      PRELIMINARY;      PRT;   555 AA.
AC   Q9SNK5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SIMILAR TO OSMLO-H1.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Sasaki T., Matsumoto T., Yamamoto K.;
RT   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 3, PAC
RT   clone:P0043E01.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AP000615; BAA85400.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
SQ   SEQUENCE   555 AA;  62685 MW;  F651FADB3B79E13C CRC64;


  Query Match             73.5%;  Score 2049.5;  DB 10;  Length 555;
  Best Local Similarity   72.1%;  Pred. No. 3.1e-188;
  Matches  403;  Conservative   49;  Mismatches   64;  Indels   43;  Gaps    8;

Qy      6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
          |   | |||||:|||||| | :||||| ||||||||||  | |||: ||||||:|||||
Db      4 GGGGRALPETPTWAVAVVCAVIVLVSVAMEHGLHKLGHWFHKREKKAMGEALEKIKAELM 63

Qy     66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK------RGTEGRKPSK-----YV--- 111
          |:|||||| | | | |:|||| | ||::| |||      :| :|:|  :     |
Db     64 LLGFISLLLTVAQTP-ISKICIPESAANIMLPCKAGQDIVKGLKGKKDHRRRLLWYTGEE 122

Qy    112 ------------DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR 157
                       ||| : |||||||:| :||||:|||||||||||| |||:|| ||||:
Db    123 ESHRRSLAGAAGEDYCAQSGKVALMSSGGMHQLHIFIFVLAVFHVTYCVITMALGRLKMK 182

Qy    158 TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTK 217
          ||||| || ||||||||||:|||||||||||||||||||||:||:|||||||| ||||
Db    183 KWKKWELETNSLEYQFANDPSRFRFTHQTSFVKRHLGLSSTPGLRWIVAFFRQFFGSVTK 242

Qy    218 VDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGV 277
          |||||:| |||||||||||||||||||||:|||||||||||||||| |||| ||||| |
Db    243 VDYLTMRQGFINAHLSQNSKFDFHKYIKRSLEDDFKVVVGISLPLWFVAILVLFLDIQGF 302

Qy    278 GTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWV 337
          ||||||||:|||||: |||||||:|||||.||||||:||||||||||||||:|||:|||||
Db    303 GTLIWISFVPLVILMLVGTKLEMVIMEMAQEIQDRATVIKGAPVVEPSNKYFWFNRPDWV 362

Qy    338 LFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLY 397
          |||||| ||||||||||||||:|||||||||:|  :|||||||||: :|||||| ||||||
Db    363 LFFIHLILFQNAFQMAHFVWTLATPGLKKCFHENMGLSIMKVVVGIFIQFLCSYSTFPLY 422

Qy    398 ALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMP 457
          |||||||||||::||:||| ||| ||| ||:|||:|| |  :||| || |        |
Db    423 ALVTQMGSNMKKTIFEEQTMKALMNWRKTAREKKKLRDADEFLAQMSGDTT--------P 474

Qy    458 SRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVA-----HPVHRLNPNDRRR 512
          |||||||||||   ||:|| ||| ||    |||||||| ||      |  :|::| |:||
Db    475 SRGSSPVHLLHKQRVRSEDPPSAPASPGFAGEARDMYPVPVAPVVRPHGFNRMDP-DKRR 533

Qy    513 SASSSALEADIPSADFSFS 531
          :|||||:: ||  :|||||
Db    534 AASSSAIQVDIADSDFSFS 552
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RESULT   6
Q93XC8
ID   Q93XC8      PRELIMINARY;      PRT;   555 AA.
AC   Q93XC8;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SEVEN TRANSMEMBRANE PROTEIN MLO2.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. IR64; TISSUE=LEAF;
RA   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane MLO family.";
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF384030; AAK94907.1; -.
KW   Transmembrane.
SQ   SEQUENCE   555 AA;  62655 MW;  F651FADB23E8683C CRC64;


  Query Match             73.4%;  Score 2046.5;  DB 10;  Length 555;
  Best Local Similarity   72.1%;  Pred. No. 5.9e-188;
  Matches  403;  Conservative   48;  Mismatches   65;  Indels   43;  Gaps    8;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |   | |||||:|||||| | :||||| ||||||||||||  | |||: |||||:|||||
Db       4 GGGGRALPETPTWAVAVVCAVIVLVSVAMEHGLHKLGHWFHKREKKAMGEALEKIKAELM 63

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK------RGTEGRKPSK-----YV--- 111
           |:|||||| | | | |:|||| | ||::| |||      :| :|:|  :     |
Db      64 LLGFISLLLTVAQTP-ISKICIPESAANIMLPCKAGQDIVKGLKGKKDHRRRLLWYTGEE 122

Qy     112 ------------DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR 157
                      ||| : ||||||:| :||||:|||||||||||| |||:|| ||||:
Db     123 ESHRRSLAGAAGEDYCAQSGKVALMSSGGMHQLHIFIFVLAVFHVTYCVITMALGRLKMK 182

Qy     158 TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTK 217
           ||||| || |||||||||:|||||||||||||||||||||:||:|||||||| ||||
Db     183 KWKKWELETNSLEYQFANDPSRFRFTHQTSFVKRHLGLSSTPGLRWIVAFFRQFFGSVTK 242

Qy     218 VDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGV 277
           ||||||| ||||||||||||||||||||:|||||||||||||| |||| ||||| |
Db     243 VDYLTMRQGFINAHLSQNSKFDFHKYIKRSLEDDFKVVVGISLPLWFVAILVLFLDIQGF 302

Qy     278 GTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWV 337
           |||||||:|||||: |||||||:||||| ||||||:||||||||||||||:|||:|||||
Db     303 GTLIWISFVPLVILMLVGTKLEMVIMEMAQEIQDRATVIKGAPVVEPSNKYFWFNRPDWV 362

Qy     338 LFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLY 397
           |||||| |||||||||||||:|||||||:|  :|||||||||: :|||||| |||||
Db     363 LFFIHLILFQNAFQMAHFVWTLATPGLKKCFHENMGLSIMKVVVGIFIQFLCSYSTFPLY 422

Qy     398 ALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMP 457
           |||||||||||::||:||| ||| ||| ||:||||:|| |  :||| || |        |
Db     423 ALVTQMGSNMKKTIFEEQTMKALMNWRKTAREKKKLRDADEFLAQMSGDTT--------P 474

Qy     458 SRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVA-----HPVHRLNPNDRRR 512
           |||||||||||||   ||:|| ||| ||    |||||||| ||      |  :| :| |:||
Db     475 SRGSSPVHLLHKQRVRSEDPPSAPASPGFAGEARDMYPVPVAPVVRPHGFNRTDP-DKRR 533

Qy     513 SASSSALEADIPSADFSFS 531
           :||||||:: ||  :|||||
Db     534 AASSSAIQVDIADSDFSFS 552


RESULT   7
Q94EX3
ID   Q94EX3      PRELIMINARY;      PRT;   554 AA.
AC   Q94EX3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MLO.
GN   MLO.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. MILYANG 117;
RA   Kim M.C., Lee S.H., Kim J.K., Chun H.J., Kim J.C., Heo W.D.,
RA   Chung W.S., Choi M.S., Park C.Y., Yoon H.W., Cho M.J.;
RT   "Isolation and characterization of Mlo homolog in rice.";
RL   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF388195; AAK72963.1; -.
SQ   SEQUENCE   554 AA;  62454 MW;  029EAC3D8F80C847 CRC64;


  Query Match             67.4%;  Score 1880;  DB 10;  Length 554;
  Best Local Similarity   67.8%;  Pred. No. 6e-172;
  Matches  379;  Conservative   55;  Mismatches   81;  Indels   44;  Gaps   11;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |   | |||||:|||||| | :||||| ||||||||||||  | |||: ||| |:|||||
Db       4 GGGGRALPETPTWAVAVVCAVIVLVSVAMEHGLHKLGHWFHKREKKAMGEALGKIKAELM 63

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK------RGTEGRKPSK-----YV--- 111
           |:|||||| | | | |:|||| | ||::| |||      :| :|:|  :     |
Db      64 LLGFISLLLTVAQTP-ISKICIPESAANIMLPCKAGQDIVKGLKGKKDHRRRLLWYTGEE 122

Qy     112 ------------DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR 157
                      ||| : ||||||:| :||||:|||||||||||| |||: | ||||:
Db     123 ESHRRSLAGAAGEDYCAQSGKVALMSSGGMHQLHIFIFVLAVFHVTYCVITMGLGRLKMK 182

Qy     158 TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLG-LSSTPGIRWVVAFFRQFFRSVT 216
           |||||::| ||||||| ||:|||||||||||||||  |||||:||:|||||||| |||
Db     183 KWKKWESQTNSLEYQFAIDPSRFRFTHQTSFVKRHLGSFSSTPGLRWIVAFFRQFFGSVT 242

Qy     217 KVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDING 276
           ||||||:| |||||||||||||||||||||:|||||||||||||| | || |||||:|
Db     243 KVDYLTMRQGFINAHLSQNSKFDFHKYIKRSLEDDFKVVVGISLPLWFVGILVLFLDIHG 302

Qy     277 VGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDW 336
           :|||||||:||:|:| |||||||:||:|| ||||||:||:|||||||||:|||:||||
Db     303 LGTLIWISFVPLIIVLLVGTKLEMVIMQMAQEIQDRATVIQGAPVVEPSNKYFWFNRPDW 362

Qy     337 VLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPL 396
           |||||||||| ||||||||||:||||||:|  | |||::|:||::|| ||||:||||
Db     363 VLFFIHLTLFHNAFQMAHFVWTMATPGLKKCFHENIWLSIVEVIVGISLQVLCSYITFPL 422

Qy     397 YALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPM 456
           |||||||||||::||:||| ||| |||  | |||||| |  :|||  |       ::|
Db     423 YALVTQMGSNMKKTIFEEQTMKALMNWRKKAMEKKKVRDADAFLAQMSVDF-----ATPA 477

Qy     457 PSRGSSPVHLLHKGMGRSDDPQSAPT--SPRTQQEARDMYPVVVAHPVHRL--NPNDRRR 512
           || :||||||     | ||| |  |  ||   :|  |:|||  |    :|  :| |||
Db     478 SSRSASPVHLLQDHRARLDDPPSPITVASPPAPEE--DIYPVPAAAAFCQLLDDPPDRRW 535

Qy     513 SASSSALEADIPSADFSFS 531
           ||   | ||||  |||||
Db     536 MAS---LSADIPDFDFSFS 551


RESULT   8
Q94CH4
ID   Q94CH4      PRELIMINARY;      PRT;   563 AA.
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AC   Q94CH4;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SEVEN TRANSMEMBRANE PROTEIN MLO1.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RA   Briggs S.P., Simmons C.R.;
RT   "Manipulation of mlo genes to enhance disease resistance in plants.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RA   Cahoon R.E., Miao G.-H., Rafalski J.A., Taramino G.;
RT   "Zea mays cDNA encoding southern corn leaf blight resistance
RT   protein.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RA   Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R.,
RA   Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane Mlo family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY029312; AAK38337.1; -.
KW   Transmembrane.
SQ   SEQUENCE   563 AA;  63086 MW;  B021C891063FF03B CRC64;
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  Query Match             61.9%;  Score 1727;  DB 10;  Length 563;
  Best Local Similarity   61.8%;  Pred. No. 3.1e-157;
  Matches  349;  Conservative   68;  Mismatches  102;  Indels   46;  Gaps   10;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |   |:|| ||:||||:| | :||||| ||||||||||  | |||: |||||:|||||
Db       4 GGGGRDLPSTPTWAVALVCAVIVLVSVAMEHGLHKLGHWFHTRQKKAMREALEKIKAELM 63

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK--RG---------TEGRK-------- 106
           |:|||||| | | | |:|||   |  :| |||  :|         ::||:
Db      64 LMGFISLLLAVGQTP-ISKICIPAKAGSIMLPCKPPKGAAAAADDDKSDGRRRLLWYPPY 122

Qy     107 -----PSKY----------VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIA 150
                 |  :           :||  :|||:|:|:  :||||:|||||||||: ||| |:|
Db     123 PGYDEPGHHRRFLAGAAPDDNYCSDQGKVSLISSAGVHQLHIFIFVLAVFHIVYSVATMA 182

Qy     151 LSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQ 210
           | ||||| ||||:|| |||||:||||:|||||||||||||||||||||:|||||||||
Db     183 LGRLKMRKWKKWESETNSLEYQYANDPSRFRFTHQTSFVKRHLGLSSTPGVRWVVAFFRQ 242

Qy     211 FFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTL 270
           || |||||||||:| |||| ||| ::||:| :|||||:|||||||||||||| ||| ||
Db     243 FFASVTKVDYLTMRQGFINYHLSPSTKFNFQQYIKRSLEDDFKVVVGISLPLWFVAIFTL 302

Qy     271 FLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFW 330
             :|| | |||:||||:|||||| || |||::||||| ||||:|:|||||||||::|||
Db     303 LIDIKGFGTLVWISFVPLVILLLVGAKLEVVIMEMAKEIQDKATVIKGAPVVEPSDRFFW 362

Qy     331 FHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCS 390
           |:|| |||| ||||          |    | |  ::    : |||||| ||| || |||
Db     363 FNRPGWVLFLIHLTALPERLPDGAFRLDTAHPRPEEMLPREAGLSIMKVAVGLVLQVLCS 422

Qy     391 YMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDT----DMLMAQMIGD 446
           |:|||||||||||:||:::||:|||:||:  || |||:| : |:     |:| :     |
Db     423 YITFPLYALVTQMGSHMKKTIFEEQTAKAVMKWRKTAKDKVRQREAAGFLDVLTS---AD 479

Qy     447 ATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLN 506
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             |||   :  ||||:||||||||  |||::||| | ||   :|  |||||   | :|||:
Db     480 TTPSHSRATSPSRGNSPVHLLHKYRGRSEEPQSGPASP--GRELGDMYPVADQHRLHRLD 537

Qy     507 PNDRRRSASSSALEADIPSADFSFS 531
           | :| | |||:|:  ||  ||||||
Db     538 P-ERMRPASSTAVNIDIADADFSFS 561


RESULT   9
Q94CG9
ID   Q94CG9      PRELIMINARY;      PRT;   515 AA.
AC   Q94CG9;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SEVEN TRANSMEMBRANE PROTEIN MLO6.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. HIII;
RA   Briggs S.P., Simmons C.R.;
RT   "Manipulation of mlo genes to enhance disease resistance in plants.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. HIII;
RA   Cahoon R.E., Miao G.-H., Rafalski J.A., Taramino G.;
RT   "Zea mays cDNA encoding southern corn leaf blight resistance
RT   protein.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. HIII;
RA   Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R.,
RA   Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane Mlo family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY029317; AAK38342.1; -.
KW   Transmembrane.
SQ   SEQUENCE   515 AA;  56984 MW;  8C61F12E7C8A0D3B CRC64;
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  Query Match             45.1%;  Score 1257;  DB 10;  Length 515;
  Best Local Similarity   48.7%;  Pred. No. 4.2e-112;
  Matches  251;  Conservative   84;  Mismatches  116;  Indels   64;  Gaps    7;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |  :||| :||:||||| |   :||:|:|:|:| ||| :| :| || ||| :|||||:|||||
Db       7 GGNSRELDQTPTWAVASVCGVIVLISILLEKGLHHVGEFFSHRKKKAMVEALEKVKAELM 66

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK-----------RGTE----------- 103
           ::|||||||:  |: || |:|||  ||: | |||           | |
Db      67 VLGFISLLLVFGQNYII-KVCISNHAANTMLPCKLEAAAVEGKDGHGKEAAAVVAGKKKV 125

Qy     104 -----GRKPSK----------YVDY-------------------CPEGKVALMSTGSLH 128
                 |:|  |           ||:                   |||||| |:|  :||
Db     126 AVAVPGKKKKKAAAAADHLGGVVDWPPPYYAHNARMLAEASMATKCPEGKVPLISINALH 185

Qy     129 QLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSF 188
           |||:||| ||||||:|| ||:|| | |:| ||:|| |    :|:|::|| ||||||:|||
Db     186 QLHIFIFFLAVFHVSYSAITMALGRAKIRAWKEWEKEAAGQDYEFSHDPTRFRFTHETSF 245

Qy     189 VKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRS 247
           |::|:  |:  |   ::  |||||||| : ||  ||  |:| ||:  ||||| ||||||
Db     246 VRQHMNVLNKFPASFYISNFFRQFFRSVRQADYCALRHSFVNVHLAPGSKFDFQKYIKRS 305

Qy     248 MEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMAL 307
           :||||||:|||| |||  |:: |||::||  |::||| :|:||:| |||||: ||  ||:
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Db    306 LEDDFKVIVGISPPLWASALIFLFLNVNGWHTMLWISIMPVVIILSVGTKLQGIICRMAI 365

Qy    308 EIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKC 367
          :| :| :||:| |:|: |: :||| || :||| || ||||| ||: :|:| :   |:  |
Db    366 DITERHAVIQGIPMVQVSDSYFWFARPTFVLFLIHFTLFQNGFQIIYFLWILYEYGMDSC 425

Qy    368 YHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTA 427
          ::       :: :|: :| ||||:| |||||:|||| ||:||||||||||| |||  |
Db    426 FNDSEEFVFARLCLGVVVQVLCSYVTLPLYALVSQMGSTMKQSIFDEQTSKALKNWRAGA 485

Qy    428 KEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS 462
          |:|         ::  |  :|: | ||  : | :
Db    486 KKKAPTGG-----SKHGGGGSPTAGGSPTKADGDA 515


RESULT  10
Q94KB3
ID   Q94KB3      PRELIMINARY;      PRT;   576 AA.
AC   Q94KB3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MEMBRANE PROTEIN MLO12.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane MLO family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF369573; AAK53805.1; -.
SQ   SEQUENCE   576 AA;  66548 MW;  43DA9F6AED64D8E6 CRC64;


  Query Match             45.0%;  Score 1255.5;  DB 10;  Length 576;
  Best Local Similarity   46.0%;  Pred. No. 6.7e-112;
  Matches  258;  Conservative   93;  Mismatches  155;  Indels   55;  Gaps   11;

Qy      7 VPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELML 66
          :  | | |||:|||||   :: :|:::|: || :|||: :||||| |||||:||||||
Db      3 IKERSLEETPTWAVAVVCFVLLFISIMIEYFLHFIGHWFKKKHKKALSEALEKVKAELML 62

Qy     67 VGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE-----------GRK--------- 106
          :|||||||:| | | :::|||  : |    ||    |           |||
Db     63 LGFISLLLVVLQTP-VSEICIPRNIAATWHPCSNHQEIAKYGKDYIDDGRKILEDFDSND 121

Qy    107 --------PSKYVDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR 157
                 :|  | | | ||||||:|   :||||:|||||||||| | :|| || : ||:
Db    122 FYSPRRNLATKGYDKCAEKGKVALVSAYGIHQLHIFIFVLAVFHVLYCIITYALGKTKMK 181

Qy    158 TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSVT 216
          || || || ::|||:|||| ||||   ||| :||| : | :    |:  |||||| |||
Db    182 KWKSWERETKTIEYQYANDPERFRFARDTSFGRRHLNIWSKSTFTLWITCFFRQFFGSVT 241

Qy    217 KVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDI 274
          |||||||| ||| |||   |  :||| |||:||:| || ||||||  :| :|:| :  :
Db    242 KVDYLTLRHGFIMAHLPAGSAARFDFQKYIERSLEQDFTVVVGISPLIWCIAVLFILTNT 301

Qy    275 NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRP 334
          :|  : :|: |:||:::| || ||:||| :: | ||::  |:|||||||| :  ||| ||
Db    302 HGWDSYLWLPFLPLIVILIVGAKLQMIISKLGLRIQEKGDVVKGAPVVEPGDDLFWFGRP 361

Qy    335 DWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTF 394
          ::|| ||| || ||||:| |||:     || |:| :     ::: :|: :| ||||:|
Db    362 RFILFLIHLVLFTNAFQLAFFVWSTYEFTLKNCFHHKTEDIAIRITMGVLIQVLCSYITL 421

Qy    395 PLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSS 454
          ||||||||||::|: :||::: : ||  | :|||:: |   :        |  ||
Db    422 PLYALVTQMGTSMRPTIFNDRVANALKKWHHTAKKQTKHGHS--------GSNTPHSSRP 473

Qy    455 PMPSRGSSPVHLLHKGMGRSDDPQ----SAPTSPRTQQEARDMYPVVVAHPVHRLNPNDR 510
            |: | |||||||    || | |    ::|: ||    :   :      |  |  :|  :
Db    474 TTPTHGMSPVHLLHNYNNRSLDQQTSFTASPSPPRFSDYSGQGH----GHQ-HFFDPESQ 528

Qy    511 RRSASSSALEADIPSADFSFS 531
            |      : :|  ::|| |
Db    529 NHS-----YQREITDSEFSNS 544


RESULT  11
Q9SXB6
ID   Q9SXB6      PRELIMINARY;      PRT;   573 AA.
AC   Q9SXB6;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T28P6.4 PROTEIN (MEMBRANE PROTEIN MLO2).
GN   T28P6.4.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN.  [1]
RP   SEQUENCE FROM N.A.
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA   Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA   Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA   Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane MLO family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC007259; AAD49991.1; -.
DR   EMBL; AF369563; AAK53795.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
SQ   SEQUENCE   573 AA;  65543 MW;  36FA911F8B1D94A6 CRC64;


  Query Match             45.0%;  Score 1253.5;  DB 10;  Length 573;
  Best Local Similarity   44.1%;  Pred. No. 1e-111;
  Matches  261;  Conservative   91;  Mismatches  161;  Indels   79;  Gaps   13;

Qy      1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
          |:|:  |  | | || :||||||   :: :|:::|| :||:| ||: :||:||:||||||:
Db      1 MADQ--VKERTLEETSTWAVAVVCFVLLFISIVLEHSIHKIGTWFKKKHKQALFEALEKV 58

Qy     61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK---------- 109
          ||||||:|||||||  : | | |: ||||:  |  | ||    | :|  |
Db     59 KAELMLLGFISLLLTIGQTP-ISNICISQKVASTMHPCSAAEEAKKYGKKDAGKKDDGDG 117

Qy    110 -------------YV----------DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTY 144
                        |:          | | | |||| :|   :||||:||||||| || |
Db    118 DKPGRRLLLELAESYIHRRSLATKGYDKCAEKGKVAFVSAYGIHQLHIFIFVLAVVHVVY 177

Qy    145 SVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRW 203
          ::| |  ::|||||| || || ::|||::||| ||||   ||| :|||   | |    |
Db    178 CIVTYAFGKIKMRTWKSWEEETKTIEYQYSNDPERFRFARDTSFGRRHLNFWSKTRVTLW 237

Qy    204 VVAFFRQFFRSVTKVDYLTLRAGFINAHLS--QNSKFDFHKYIKRSMEDDFKVVVGISLP 261
          :| |||||| |||||||| || ||| || :    |:||| |||:||:| ||| || ||
Db    238 IVCFFRQFFGSVTKVDYLALRHGFIMAHFAPGNESRFDFRKYIQRSLEKDFKTVVEISPV 297

Qy    262 LWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPV 321
          :| ||:| |  :  |: : :|: ||||||:| |||||||| :: | ||::  |::||||
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Db    298 IWFVAVLFLLTNSYGLRSYLWLPFIPLVVILIVGTKLEVIITKLGLRIQEKGDVVRGAPV 357

Qy    322 VEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVV 381

Db    358 VQPGDDLFWFGKPRFILFLIHLVLFTNAFQLAFFAWSTYEFNLNNCFHESTADVVIRLVV 417

Qy    382 GLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMA 441

Db    418 GAVVQILCSYVTLPLYALVTQMGSKMKPTVFNDRVATALKKWHHTAKNETK-------HG 470

Qy    442 QMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHP 501

Db    471 RHSGSNTPFSSRPTTPTHGSSPIHLLHNFNNRS--VENYPSSPSPRYSGH-------GHH 521

Qy    502 VHRL-NPNDRRRSASSS-----ALEADIP--------------SADFSFSQ 532

Db    522 EHQFWDPESQHQEAETSTHHSLAHESSEPVLASVELPPIRTSKSLRDFSFKK 573


RESULT  12
Q9SY94
ID   Q9SY94      PRELIMINARY;      PRT;   583 AA.
AC   Q9SY94;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   T25B24.9 PROTEIN.
GN   T25B24.9.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RA   Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
RA   Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
RA   Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S.,
RA   Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S.,
RA   Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL   Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC005850; AAD25552.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
SQ   SEQUENCE   583 AA;  67226 MW;  E6A3683CA8BB9150 CRC64;


  Query Match             44.3%;  Score 1234.5;  DB 10;  Length 583;
  Best Local Similarity   43.6%;  Pred. No. 7.2e-110;
  Matches  261;  Conservative   97;  Mismatches  159;  Indels   81;  Gaps   12;

Qy      1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60

Db      1 MADQ--VKEKTLEETSTWAVAVVCFVLLLISIVIEKLIHKIGSWFKKKNKKALYEALEKV 58

Qy     61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRK---------------- 106

Db     59 KAELMLMGFISLLLTIGQG-YISNICIPKNIAASMHPCSASEEARKYGKKDVPKEDEEEN 117

Qy    107 -----------------PSKYVDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVI 147

Db    118 LRRKLLQLVDSLIPRRSLATKGYDKCAEKGKVAFVSAYGMHQLHIFIFVLAVCHVIYCIV 177

Qy    148 TIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-WVVA 206

Db    178 TYALGKTKMRRWKKWEEETKTIEYQYSHDPERFRFARDTSFGRRHLSFWSKSTITLWIVC 237

Qy    207 FFRQFFRSVTKVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWG 264

Db    238 FFRQFFRSVTKVDYLTLRHGFIMAHLAPGSDARFDFRKYIQRSLEEDFKTIVEINPVIWF 297

Qy    265 VAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEP 324

Db    298 IAVLFLLTNTNGLNSYLWLPFIPFIVILIVGTKLQVIITKLGLRIQEKGDVVKGTPLVQP 357

Qy    325 SNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLA 384

Db    358 GDHFFWFGRPRFILFLIHLVLFTNAFQLAFFVWSTYEFGLKNCFHESRVDVIIRISIGLL 417

Qy    385 LQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMI 444

Db    418 VQILCSYVTLPLYALVTQMGSKMKPTVFNERVATALKSWHHTAKKNIKHGRTS------- 470

Qy    445 GDATPSRGSSPMPSRGSSPVHLL----HKGMGRSDDPQSAPTSPR----------TQQEA 490

Db    471 ESTTPFSSRPTTPTHGSSPIHLLRNAPHKRSRSVDESFANSFSPRNSDFDSWDPESQHET 530

Qy    491 RDMYPVVVAHPVH--RLNPNDRRRSASSSALE-------------ADIPSADFSFSQ 532

Db    531 AE-----TSNSNHRSRFGEEESEKKFVSSSVELPPGPGQIRTQHEISTISLRDFSFKR 583


RESULT  13
Q94KB7
ID   Q94KB7      PRELIMINARY;      PRT;   583 AA.
AC   Q94KB7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   MEMBRANE PROTEIN MLO6.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane MLO family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF369567; AAK53799.1; -.
SQ   SEQUENCE,  583 AA;  67097 MW;  4DA8683CA8BC5C5D CRC64;


  Query Match             43.8%;  Score 1221.5;  DB 10;  Length 583;
  Best Local Similarity   43.5%;  Pred. No. 1.3e-108;
  Matches  260;  Conservative   97;  Mismatches  160;  Indels   81;  Gaps   12;

Qy      1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60

Db      1 MADQ--VKEKTLEETSTWAVAVVCFVLLLISIVIEKLIHKIGSGFKKKNKKALYEALEKV 58

Qy     61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRK---------------- 106

Db     59 KAELMLMGFISLLLTIGQG-YISNICIPKNIAASMHPCSASEEARKYGKKDVPKEDEEEN 117

Qy    107 -----------------PSKYVDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVI 147

Db    118 LRRKLLQLVDSLIPRRSLATKGYDKCAEKGKVAFVSAYGMHQLHIFIFVLAVCHVIYCIV 177

Qy    148 TIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-WVVA 206

Db    178 TYALGKTKMRRWKKWEEETKTIEYQYSHDPERFRFARDTSFGRRHLSFWSKSTITLWIVC 237

Qy    207 FFRQFFRSVTKVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWG 264

Db    238 FFRQFFRSVTKVDYLTLRHGFIMAHLAPGSDARFDFRKYIQRSLEEDFKTIVEINPVIWF 297

Qy    265 VAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEP 324

Db    298 IAVLFLLTNTNGLNSYLWLPFIPFIVILIVGTKLQVIITKLGLRIQEKGDVVKGTPLVQP 357

Qy    325 SNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLA 384
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Db    358 GDHFFWFGRPRFILFLIHLVLFTNAFQLAFFVWSTYEFGLKNCFHESRVDVIIRISIGLL 417

Qy    385 LQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMI 444

Db    418 VQILCSYVTLPLYALVTQMGSKMKPTVFNERVATALKSWHHTAKKNIKHGRTS------- 470

Qy    445 GDATPSRGSSPMPSRGSSPVHLL----HKGMGRSDDPQSAPTSPR----------TQQEA 490

Db    471 ESTTPFSSRPTTPTHGSSPIHLLRNAPHKRSRSVDESFANSFSPRNSDFDSWDPESQHET 530

Qy    491 RDMYPVVVAHPVH--RLNPNDRRRSASSSALE-------------ADIPSADFSFSQ 532

Db    531 AE-----TSNSNHRSRFGEEESEKKFVSSSVELPPGPGQIRTQHEISTISLRDFSFKR 583


RESULT  14
Q9FRJ3
ID   Q9FRJ3      PRELIMINARY;      PRT;   580 AA.
AC   Q9FRJ3;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   PUTATIVE MLO (PATHOGEN RESISTANCE) PROTEIN.
GN   OSJNBB0064P21.5.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. NIPPONBARE;
RA   Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,
RA   Zismann V., Pai G., Bowman C.L., Fujii C.Y., VanAken S.E.,
RA   Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblyum T.V.,
RA   Quackenbush J., White O., Salzberg S.L., Fraser C.M.;
RT   "Oryza sativa chromosome 10 BAC OSJNBb0064P21 genomic sequence.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AC073166; AAG46114.1; -.
SQ   SEQUENCE   580 AA;  64796 MW;  CD263AD8F8C350FC CRC64;


  Query Match             42.8%;  Score 1192;  DB 10;  Length 580;
  Best Local Similarity   47.1%;  Pred. No. 8.6e-106;
  Matches  253;  Conservative   80;  Mismatches  146;  Indels   58;  Gaps   10;

Qy      6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65

Db     14 GDGARALDQTPTWAVAAVCAVIVAASILLEGLLHHLGQWFSKRRKKALFDALEKVKSELM 73

Qy     66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK-----------RGTEGRK-----PS 108

Db     74 TLGFISLLLSVT-GRYISRICIPVGAADTMLPCSLRRSSSEQEVPGGGGHGRRHLSGDPT 132

Qy    109 KYVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTS 168

Db    133 NF--KCAKGMVSLVSADGLHQLHIFVFFLAVFHVAFSAITMSLGRAKTRIWKEWEKETCS 190

Qy    169 LEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGF 227

Db    191 LTYEFSYDPSKFRLTHQTSFVRQHASCWSKSTILLYFVSFFRQFFRSVRRTDYLTLRHGF 250

Qy    228 INAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIP 287

Db    251 IAAHLSLGTRFNFRKYIKRSLEDDFKTVVGISAPLWASALAIMLFNVHGWHNLFWFSTIP 310

Qy    288 LVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQ 347

Db    311 LVVTLAVGTKLQAIIAMMAVEIKERHTVIQGMPVVKLSDEHFWFGKPRLVLHLIHFASFQ 370

Qy    348 NAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNM 407

Db    371 NAFEITYFFWIWYEFGLRSCFHDNFELIIARVCLGVVVQFMCSYITLPLYALVSQMGSQM 430

Qy    408 KRSIFDEQTSKALTNWRNTAKEKKKVR-------------DTDMLMAQMIGDATPSRGS 453

Db    431 KRTIFDEQTAKALKKWHKAAVVKKKQQKGSSHEPGSETPGTETTTTTATATEESQRERDA 490

Qy    454 SPMPSRGSSPVHL------LHKG---------MGRSDDPQSAPTS---PRTQQEARD 492

Db    491 AAMPVR-----HLHRYKTIAHVGATGTLSDSDCSDTDTPFASPTRLLIPPTKQRSLD 542


RESULT  15
Q94CH3
ID   Q94CH3      PRELIMINARY;      PRT;   565 AA.
AC   Q94CH3;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   SEVEN TRANSMEMBRANE PROTEIN MLO2.
OS   Zea mays (Maize).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC   Panicoideae; Andropogoneae; Zea.
OX   NCBI_TaxID=4577;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RA   Briggs S.P., Simmons C.R.;
RT   "Manipulation of mlo genes to enhance disease resistance in plants.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. B73;
RA   Devoto A., Hartmann A., Piffanelli P., Elliott C., Simmons C.R.,
RA   Taramino G., Goh C.-S., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the plant-
RT   specific seven transmembrane Mlo family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY029313; AAK38338.1; -.
KW   Transmembrane.
SQ   SEQUENCE   565 AA;  64278 MW;  ADEA5EE7331F7407 CRC64;


  Query Match             41.6%;  Score 1160;  DB 10;  Length 565;
  Best Local Similarity   44.5%;  Pred. No. 9.9e-103;
  Matches  253;  Conservative   81;  Mismatches  174;  Indels   60;  Gaps   11;

Qy      6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65

Db      3 GDGTRALDQTPTWAVAAVCAVIVAASILLEGFLHHLGQLLNKKRKKALFDALEKVKSELM 62

Qy     66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK----------RGTEGRK-----PSKY 110

Db     63 TLGFISLLLTVT-GRYIARICIPEGAANTMLPCRLSGHSVAEEPKG-HGRRHLSEDPTNL 120

Qy    111 VDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLE 170

Db    121 FS-CRKGMVSLVSADGMHQLHIFVFFLAVFHVTFSFFTMSLGRAKTRIWKVWEKETCSPQ 179

Qy    171 YQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-WVVAFFRQFFRSVTKVDYLTLRAGFIN 229

Db    180 YNYLNDPSKFRLTHQTSFVRQHASCWSKSTITLYFVSFFRQFFRSVRKTDYFTLRHGFIS 239

Qy    230 AHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLV 289

Db    240 AHLSPGTRFNFRKYIKRSLEDDFKTVVGISPPLWASALAVMLFNVHGWHNLFWFSAIPLV 299

Qy    290 ILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNA 349

Db    300 VILAVGTKLQAIIAMMAIEIAERHTVIQGMPVVKLSDDHFWFGKPRLVLHLIHFASFQNA 359

Qy    350 FQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKR 409
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```
Db    360 FEITYFFWIWYEFGLRSCFHDNFEFIIARVCLGAIVQFMCSYITLPLYALVSQMGSEMKR 419

Qy    410 SIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS------- 462
          :||||||:|||  |     :||  :|:             |  ||  ||  ::
Db    420 TIFDEQTAKALKKWHKAVVKKKHHKDS------------SHNSSETPSTDTTGPAGEAG 466

Qy    463 --------PVHLLHK-----GMGRSDDPQSAP-------TSPRTQQEARDMYPVVVAHPV 502
                  ||  ||:      :|    | | |       | | : |  | : |      :
Db    467 EWQRLHEVPVRHLHRYKTIAHVGGVRSPLSDPDYSDTDDTEPLSLQ-TRHLIPPAKQRSL 525

Qy    503 HRLNPNDRRRSASSSALEADIPSADFSF 530
                |     ::|  :|:    |||
Db    526 DTERAEVRVNVVETAAAPSDVLQDSFSF 553


Search completed: July 23, 2002, 14:32:55
Job time: 495 sec
```

GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 23, 2002, 14:25:25 ; Search time 25.02 Seconds
(without alignments)
824.841 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSSALEADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2788	100.0	533	1	MLO_HORVU	P93766 hordeum vul
2	1941	69.6	544	1	MLH1_HORVU	O49873 hordeum vul
3	1792	64.3	537	1	MLH1_ORYSA	O49914 oryza sativ
4	1220.5	43.8	570	1	YML6_ARATH	O80961 arabidopsis
5	1101.5	39.5	501	1	MLO5_ARATH	O22815 arabidopsis
6	1061	38.1	580	1	YML1_ARATH	O22752 arabidopsis
7	1039	37.3	560	1	YML2_ARATH	O22757 arabidopsis
8	932.5	33.4	526	1	MLO1_ARATH	O49621 arabidopsis
9	927	33.2	496	1	ML15_ARATH	O80580 arabidopsis
10	499.5	17.9	447	1	YML3_ARATH	O23693 arabidopsis
11	429	15.4	217	1	MLOL_LINUS	P81785 linum usita
12	102.5	3.7	574	1	YHGE_ECOLI	P45804 escherichia
13	95.5	3.4	443	1	HSLU_HELPJ	Q9zlw1 helicobacte
14	95.5	3.4	506	1	NFIC_PIG	P21999 sus scrofa
15	94.5	3.4	338	1	YD49_THEMA	Q9x170 thermotoga
16	94	3.4	395	1	Y306_MYCPN	P75343 mycoplasma
17	93.5	3.4	339	1	STEA_HUMAN	Q9uhe8 homo sapien
18	93.5	3.4	369	1	Y316_MYCGE	P47558 mycoplasma
19	93.5	3.4	443	1	HSLU_HELPY	O25254 helicobacte
20	93	3.3	1278	1	NPC1_HUMAN	O15118 homo sapien
21	92.5	3.3	262	1	COX3_ANOGA	P34842 anopheles g
22	92.5	3.3	262	1	COX3_DROYA	P00418 drosophila
23	92.5	3.3	439	1	NFIC_MOUSE	P70255 mus musculu
24	92	3.3	2376	1	YIM9_YEAST	P40468 saccharomyc
25	91.5	3.3	262	1	COX3_DROME	P00417 drosophila
26	91	3.3	439	1	IOLF_BACSU	P42417 bacillus su
27	91	3.3	762	1	AVP3_HORVU	Q06572 hordeum vul
28	90.5	3.2	508	1	NFIC_HUMAN	P08651 homo sapien
29	90.5	3.2	1203	1	YT41_CAEEL	Q11069 caenorhabdi
30	89.5	3.2	3079	1	IRA2_YEAST	P19158 saccharomyc
31	89	3.2	348	1	FML1_GORGO	P79177 gorilla gor
32	89	3.2	1407	1	CYAA_DICDI	Q03100 dictyosteli
33	88.5	3.2	838	1	P_HUMAN	Q04671 homo sapien
34	88.5	3.2	970	1	Y277_MYCGE	Q49409 mycoplasma
35	88	3.2	564	1	Y61A_MYCPN	P75041 mycoplasma
36	87.5	3.1	351	1	FML1_HUMAN	P25090 homo sapien
37	87.5	3.1	568	1	PTLB_STRMU	P50976 streptococc
38	87.5	3.1	587	1	T9S3_MOUSE	Q9et30 mus musculu
39	87	3.1	1012	1	DPOL_HSV7J	P52342 human herpe
40	87	3.1	1333	1	YN99_YEAST	P53756 saccharomyc
41	87	3.1	1835	1	CCAI_RAT	Q9z0y8 rattus norv
42	86.5	3.1	348	1	FML1_PONPY	P79236 pongo pygma
43	86.5	3.1	589	1	T9S3_HUMAN	Q9hd45 homo sapien
44	86	3.1	384	1	AAPM_RHILV	Q52814 rhizobium l
45	86	3.1	622	1	AMT3_CAEEL	Q21565 caenorhabdi

ALIGNMENTS

```
RESULT   1
MLO_HORVU
ID   MLO_HORVU      STANDARD;      PRT;   533 AA.
AC   P93766;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   MLO protein.
GN   MLO.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS.
RC   STRAIN=VARIOUS STRAINS; TISSUE=Leaf;
RX   MEDLINE=97207016; PubMed=9054509;
RA   Bueschges R., Hollricher K., Panstruga R., Simons G., Wolter M.,
RA   Frijters A., van Daelen R., van de Lee T., Diergaarde P.,
RA   Groenendijk J., Toepsch S., Vos P., Salamini F., Schulze-Lefert P.;
RT   "The barley Mlo gene: a novel control element of plant pathogen
RT   resistance.";
RL   Cell 88:695-705(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. INGRID;
RX   MEDLINE=98128007; PubMed=9461468;
RA   Panstruga R., Buschges R., Piffanelli P., Schulze-Lefet P.;
RT   "A contiguous 60 kb genomic stretch from barley reveals molecular
RT   evidence for gene islands in a monocot genome.";
RL   Nucleic Acids Res. 26:1056-1062(1998).
CC   -!- FUNCTION: MAY BE INVOLVED IN DOWN-REGULATING LEAF CELL DEATH AND
CC       PATHOGEN DEFENSE FUNCTIONS.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- MISCELLANEOUS: REF.1 HAS SEQUENCED MLO IN STRAINS CV. CARLSBERG
CC       II, CV. DIAMANT, CV. FOMA, CV. HAISA, CV. INGRID, CV. MALTERIA
CC       HEDA, AND CV. PLENA.
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; Z83834; CAB06083.1; -.
DR   EMBL; Y14573; CAA74909.1; -.
DR   Mendel; 13060; HORvu;2260;1.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane; Pathogenesis-related protein.
FT   TRANSMEM     18     38       POTENTIAL.
FT   TRANSMEM     63     83       POTENTIAL.
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FT   TRANSMEM     132     152       POTENTIAL.
FT   TRANSMEM     252     272       POTENTIAL.
FT   TRANSMEM     274     294       POTENTIAL.
FT   TRANSMEM     380     400       POTENTIAL.
FT   MUTAGEN       10      10       R->W: IN MLO-9; CONFERS BROAD SPECTRUM
FT                                  RESISTANCE TO POWDERY MILDEW FUNGUS.
FT   MUTAGEN       30      30       V->E: IN MLO-13; CONFERS BROAD SPECTRUM
FT                                  RESISTANCE TO POWDERY MILDEW FUNGUS.
FT   MUTAGEN       31      31       S->F: IN MLO-17; CONFERS BROAD SPECTRUM
FT                                  RESISTANCE TO POWDERY MILDEW FUNGUS.
FT   MUTAGEN      162     162       W->R: IN MLO-1; CONFERS BROAD SPECTRUM
FT                                  RESISTANCE TO POWDERY MILDEW FUNGUS.
FT   MUTAGEN      182     183       MISSING: IN MLO-10; CONFERS BROAD
FT                                  SPECTRUM RESISTANCE TO POWDERY MILDEW
FT                                  FUNGUS.
FT   MUTAGEN      226     226       G->D: IN MLO-7; CONFERS BROAD SPECTRUM
FT                                  RESISTANCE TO POWDERY MILDEW FUNGUS.
FT   MUTAGEN      270     270       L->H: IN MLO-26; CONFERS BROAD SPECTRUM
FT                                  RESISTANCE TO POWDERY MILDEW FUNGUS.
SQ   SEQUENCE   533 AA;  60412 MW;  AC0D832EE14F7D15 CRC64;


  Query Match           100.0%;  Score 2788;  DB 1;  Length 533;
  Best Local Similarity  100.0%;  Pred. No. 4.8e-227;
  Matches  533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120

Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420

Qy     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480

Qy     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533


RESULT   2
MLH1_HORVU
ID   MLH1_HORVU     STANDARD;      PRT;   544 AA.
AC   O49873;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   MLO protein homolog 1.
GN   MLO-H1.
OS   Hordeum vulgare (Barley).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
OC   Triticeae; Hordeum.
OX   NCBI_TaxID=4513;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. IGRI;
RA   Panstruga R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z95496; CAB08860.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane.
FT   TRANSMEM      16      36       POTENTIAL.
FT   TRANSMEM     285     305       POTENTIAL.
FT   TRANSMEM     403     423       POTENTIAL.
SQ   SEQUENCE   544 AA;  60875 MW;  D4FBCDD2A2A87796 CRC64;


  Query Match           69.6%;  Score 1941;  DB 1;  Length 544;
  Best Local Similarity  69.5%;  Pred. No. 9.8e-156;
  Matches  381;  Conservative   51;  Mismatches   76;  Indels   40;  Gaps    6;

Qy      10 RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGF 69
           ||| :||:|||||| | |:|||| ||| |||||||    |||| ||||||||||||||
Db       8 RELSDTPTWAVAVVCAVMILVSVAMEHALHKLGHWFHKWRKKALGEALEKMKAELMLVGF 67

Qy      70 ISLLLIVTQDPIIAKICISEDAADVMWPCK--------RGTEGRKPSKY---------- 110
           |||||||||||| :::|||::| : | |||        :| :  :   :
Db      68 ISLLLIVTQDP-VSRICISKEAGEKMLPCKPYDGAGGGKGKDNHRRLLWLQGESETHRRF 126

Qy     111 ------VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWE 163
                 || |  :|||||| ||:||||:|||||||||| |||:|: ||||||: |||||
Db     127 LAAPAGVDVCAKQGKVALMSAGSMHQLHIFIFVLAVFHVLYSVVTMTLSRLKMKQWKKWE 186

Qy     164 TETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTL 223
           :|| |||||||||:| |||||: |:|||||||||:|||||||||| |||||||||
Db     187 SETASLEYQFANDPSRCRFTHQTTLVRRHLGLSSTPGVRWVVAFFRQFFTSVTKVDYLTL 246

Qy     224 RAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWI 283
           | ||||||||| ::|||||||||:|||||||| ||| || ||:| |||| :|:|||:|:
Db     247 RQGFINAHLSQGNRFDFHKYIKRSLEDDFKVVVRISLKLWFVAVLILFLDFDGIGTLLWM 306

Qy     284 SFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHL 343
           | :|||||| |||||||:|||| || || ||:|||| ||||||:|||:|||||| :||
Db     307 SVVPLVILLWVGTKLEMVIMEMAQEIHDRESVVKGAPAVEPSNKYFWFNRPDWVLFLMHL 366

Qy     344 TLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQM 403
           |||||||||||||||||||||||| :: :|| |||:|:| | ||||:|||||||||||
Db     367 TLFQNAFQMAHFVWTVATPGLKKCYHEKMAMSIAKVVLGVAAQILCSYITFPLYALVTQM 426

Qy     404 GSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP 463
           ||:||||||||||:|||||||  |||||| ||  |||||| | ||         || ||||
Db     427 GSHMKRSIFDEQTAKALTNWRKMAKEKKKARDAAMLMAQMGGGAT--------PSVGSSP 478

Qy     464 VHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADI 523
           ||||||   ||||||| | ||| ::|        | ||  :: | |  ||||| ||:| |
Db     479 VHLLHKAGARSDDPQSVPASPRAEKEGGG-----VQHPARKVPPCDGWRSASSPALDAHI 533

Qy     524 PSADFSFS 531
           | ||| ||
Db     534 PGADFGFS 541
```

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RESULT   3
MLH1_ORYSA
ID   MLH1_ORYSA     STANDARD;      PRT;   537 AA.
AC   O49914;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   MLO protein homolog 1.
GN   MLO-H1.
OS   Oryza sativa (Rice).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC   Ehrhartoideae; Oryzeae; Oryza.
OX   NCBI_TaxID=4530;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. IR-BB21;
RA   Panstruga R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z95353; CAB08606.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane.
FT   TRANSMEM     17     37       POTENTIAL.
FT   TRANSMEM     48     68       POTENTIAL.
FT   TRANSMEM    140    160       POTENTIAL.
FT   TRANSMEM    263    283       POTENTIAL.
FT   TRANSMEM    381    401       POTENTIAL.
SQ   SEQUENCE   537 AA;  60077 MW;  EE16772A9637416B CRC64;

  Query Match             64.3%;  Score 1792;  DB 1;  Length 537;
  Best Local Similarity   67.2%;  Pred. No. 3.4e-143;
  Matches  366;  Conservative   54;  Mismatches   85;  Indels   40;  Gaps   12;

Qy       9 ARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEAL----EKMKAEL 64
           :|||||||:|||||| | :||||  |||||| | |       |   | |          |||
Db       8 SRELPETPTWAVAVVCAVLVLVSAAMEHGLHNLSH-------KTTAEVLIFLVLSALAEL 60

Qy      65 MLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE--------GRKPSKYV---DY 113
           ||:|||||| | | | |:|||| : ||::: ||| | :         ||:         ||
Db      61 MLLGFISLLLTVAQAP-ISKICIPKSAANILLPCKAGQDAIEEEAASGRRSLAGAGGGDY 119

Qy     114 CP--EGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEY 171
           |   :|||||||  |:||||:||||||||||||| :||: | ||||: |||||::| ||||
Db     120 CSKFDGKVALMSAKSMHQLHIFIFVLAVFHVTYCIITMGLGRLKMKKWKKWESQTNSLEY 179

Qy     172 QFANDPARFRFTHQTSFVKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINA 230
           ||| ||:|||||||||||||||  |||||:||:||||||| |||||||||:| |||||
Db     180 QFAIDPSRFRFTHQTSFVKRHLGSFSSTPGLRWIVAFFRQFFGSVTKVDYLTMRQGFINA 239

Qy     231 HLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVI 290
           |||||||||||||||||:|||||||||||||| | || |||||:|:|||||||||:||:|
Db     240 HLSQNSKFDFHKYIKRSLEDDFKVVVGISLPLWFVGILVLFLDIHGLGTLIWISFVPLII 299

Qy     291 LLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAF 350
           :| |||||||:||||| ||||||:||:|||:|||||||:|||:|||||||||||||| |||
Db     300 VLLVGTKLEMVIMEMAQEIQDRATVIQGAPMVEPSNKYFWFNRPDWVLFFIHLTLFHNAF 359

Qy     351 QMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRS 410
           ||||||||:|||||||:|:|||:|||| |||::|:||::|| ||||:|||||||||||||::
Db     360 QMAHFVWTMATPGLKKCFHENIWLSIVEVIVGISLQVLCSYITFPLYALVTQMGSNMKKT 419

Qy     411 IFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKG 470
           ||:||| ||| |||  | |||||||  |  :|||  |       ::|  || :||||||
Db     420 IFEEQTMKALMNWRKKAMEKKKVRDADAFLAQMSVDF-----ATPASSRSASPVHLLQDH 474

Qy     471 MGRSDDPQSAPT--SPRTQQEARDMYPVVVAHPVHRL--NPNDRRRSASSSALEADIPSA 526
           |||||  |  |  ||   :|  |||||  |    :|  :| |||  ||||   |||  :
Db     475 RARSDDPPSPITVASPPAPEE--DMYPVPAAAASRQLLDDPPDRRWMASSS---ADIADS 529

Qy     527 DFSFS 531
           |||||
Db     530 DFSFS 534


RESULT   4
YML6_ARATH
ID   YML6_ARATH     STANDARD;      PRT;   570 AA.
AC   O80961;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical MLO-like protein At2g39200.
GN   AT2G39200 OR T16B24.16.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC004697; AAC28997.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     14     34       POTENTIAL.
FT   TRANSMEM    156    176       POTENTIAL.
FT   TRANSMEM    273    293       POTENTIAL.
FT   TRANSMEM    303    323       POTENTIAL.
FT   TRANSMEM    357    377       POTENTIAL.
FT   TRANSMEM    400    420       POTENTIAL.
SQ   SEQUENCE   570 AA;  65765 MW;  4C49FBF806F90910 CRC64;

  Query Match             43.8%;  Score 1220.5;  DB 1;  Length 570;
  Best Local Similarity   45.3%;  Pred. No. 4.7e-95;
  Matches  254;  Conservative   93;  Mismatches  153;  Indels   61;  Gaps   12;
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Qy       7 VPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELML 66
           :  | | |||:|||||   :: :|:::|: || :|||| :|||| |||||:||||||
Db       3 IKERSLEETPTWAVAVVCFVLLFISIMIEYFLHFIGHWFKKKHKKALSEALEKVKAELML 62

Qy      67 VGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE----------GRK--------- 106
           :|||||||:| | | :::|||  : |    ||     |           |||
Db      63 LGFISLLLVVLQTP-VSEICIPRNIAATWHPCSNHQEIAKYGKDYIDDGRKILEDFDSND 121

Qy     107 --------PSKYVDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMR 157
                 :|  | | | |||||:|   :||||:|||||||||| | :|| || : ||:
Db     122 FYSPRRNLATKGYDKCAEKGKVALVSAYGIHQLHIFIFVLAVFHVLYCIITYALGKTKMK 181

Qy     158 TWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSVT 216
           || || || ::|||:|||| ||||   ||| :||| : | :    |:      || |||
Db     182 KWKSWERETKTIEYQYANDPERFRFARDTSFGRRHLNIWSKSTPTLWI------FFGSVT 235

Qy     217 KVDYLTLRAGFINAHLSQNS--KFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDI 274
           |||||||| ||| |||   |  :||| |||:||:| || |||||  :| :|:| :  :
Db     236 KVDYLTLRHGFIMAHLPAGSAARFDFQKYIERSLEQDFTVVVGISPLIWCIAVLFILTNT 295

Qy     275 NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRP 334
           :|  : :|: |:||:::| || ||:||| :: | ||::  |:||||||| :  ||| ||
Db     296 HGWDSYLWLPFLPLIVILIVGAKLQMIISKLGLRIQEKGDVVKGAPVVEPGDDLFWFGRP 355

Qy     335 DWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTF 394
           ::|| ||| || ||||:| |||:     || |:| :     ::: :|: :| ||||:|
Db     356 RFILFLIHLVLFTNAFQLAFFVWSTYEFTLKNCFHHKTEDIAIRITMGVLIQVLCSYITL 415

Qy     395 PLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSS 454
           ||||||||||::|: :||::: : ||  | :|||:: |   :         |  ||
Db     416 PLYALVTQMGTSMRPTIFNDRVANALKKWHHTAKKQTKHGHS--------GSNTPHSSRP 467

Qy     455 PMPSRGSSPVHLLHKGMGRSDDPQ----SAPTSPRTQQEARDMYPVVVAHPVHRLNPNDR 510
             |: | |||||||    || | |    ::|: ||    :   :     | |  :|  :
Db     468 TTPTHGMSPVHLLHNYNNRSLDQQTSFTASPSPPRFSDYSGQGH----GHQ-HFFDPESQ 522

Qy     511 RRSASSSALEADIPSADFSFS 531
             |      : :|  ::|| |
Db     523 NHS-----YQREITDSEFSNS 538


RESULT   5
MLO5_ARATH
ID   MLO5_ARATH     STANDARD;      PRT;   501 AA.
AC   O22815;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   MLO-like protein 5 (AtMlo5).
GN   MLO5 OR AT2G33670 OR F4P9.44 OR T01B08.26.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the
RT   plant-specific seven transmembrane MLO family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF369566; AAK53798.1; -.
DR   EMBL; U78721; AAC69142.2; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane; Multigene family.
FT   TRANSMEM     23     43       POTENTIAL.
FT   TRANSMEM     69     89       POTENTIAL.
FT   TRANSMEM    152    172       POTENTIAL.
FT   TRANSMEM    274    294       POTENTIAL.
FT   TRANSMEM    296    316       POTENTIAL.
FT   TRANSMEM    360    380       POTENTIAL.
FT   TRANSMEM    392    412       POTENTIAL.
FT   CONFLICT    458    458       MISSING (IN REF. 1).
SQ   SEQUENCE   501 AA;  56896 MW;  4B3F95D0FB18DCF8 CRC64;


  Query Match             39.5%;  Score 1101.5;  DB 1;  Length 501;
  Best Local Similarity   44.2%;  Pred. No. 4.1e-85;
  Matches  229;  Conservative   88;  Mismatches  140;  Indels   61;  Gaps   10;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |   ||| :||:|||: |   ::|:|:::|  :||:|  |  | ||||:|||:|:| |||
Db      11 GEGPRELDQTPTWAVSTVCGVIILISIVLELMIHKIGEVFTERRKKALYEALQKIKNELM 70

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPC----KRGTEGRKP--SKYVD------- 112
           ::|||||||   |:  || :|::      |  |        | :||  :::::
Db      71 VLGFISLLLTFGQN-YIASLCVASRYGHAMSFCGPYDGPSGESKKPKTTEHLERRVLADA 129

Qy     113 ---YCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSL 169
               | :| | |:|  :|||:|:||| |||||| || ||: | | |:| || || |  :
Db     130 APAQCKKGYVPLISLNALHQVHIFIFFLAVFHVIYSAITMMLGRAKIRGWKVWEEEVIN- 188

Qy     170 EYQFANDPARFRFTHQTSFVKRHLGLSSTPGIR-----WVVAFFRQFFRSVTKVDYLTLR 224
           :::  |||:||| ||:|||: |:     |  :     :|: |||  ||| | ||||:|
Db     189 DHEMMNDPSRFRLTHETSFVREHV----NPWAKNRFSFYVMCFFRQMLRSVRKSDYLTMR 244

Qy     225 AGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWIS 284
           |||: ||:   ||:| ||||||:|||||||||||  ||   :| |  |::|     |:
Db     245 HGFISVHLAPGMKFNFQKYIKRSLEDDFKVVVGISPELWAFVMLFLLFDVHGWYVTAVIT 304

Qy     285 FIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLT 344
           || :: | :|||: || :|||||:| :||:| |:|  |:: ||| ||  ||  ||
Db     305 MIPPLLTLAIGTKLQAIISDMALEIQERHAVIQGMPLVNVSDRHFWFSRPALVLHIIHFI 364

Qy     345 LFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMG 404
           ||||||:: :| |     ||: |:|    | |::| :|: :||||||:| ||||||||||
Db     365 LFQNAFEITYFFWIWYEFGLRSCFHHHFALIIIRVALGVGVQFLCSYITLPLYALVTQMG 424

Qy     405 SNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPS------ 458
           | ||||:||:|||||| ||   ||:| :                 || :   |:|:
Db     425 STMKRSVFDDQTSKALKNWHKNAKKKSE--------------TPGQTQPPLPNLRPKTG 469

Qy     459 ---RGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDM 493
               :|| ::           |      | ::||:
Db     470 GDIESASPANI----------TASVDVKESDQSQSRDL 497


RESULT   6
```

```
YML1_ARATH
ID   YML1_ARATH     STANDARD;      PRT;   580 AA.
AC   O22752;
DT   15-JUL-1999 (Rel. 38, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical MLO-like protein At2g17430.
GN   AT2G17430 OR F5J6.19.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC002329; AAB86520.2; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     39     59       POTENTIAL.
FT   TRANSMEM     62     82       POTENTIAL.
FT   TRANSMEM    196    216       POTENTIAL.
FT   TRANSMEM    258    278       POTENTIAL.
FT   TRANSMEM    319    339       POTENTIAL.
FT   TRANSMEM    346    366       POTENTIAL.
FT   TRANSMEM    445    465       POTENTIAL.
SQ   SEQUENCE   580 AA;  66723 MW;  AEF812A531E7EDAF CRC64;


  Query Match             38.1%;  Score 1061;  DB 1;  Length 580;
  Best Local Similarity   45.7%;  Pred. No. 1.3e-81;
  Matches  220;  Conservative   75;  Mismatches  130;  Indels   56;  Gaps    8;

Qy       6 GVPA--RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGH---------------------- 43
           | |:  :|| :||:||||||   ::|:| |:| || :| :
Db      25 GAPSGGKELSQTPTWAVAVVCTFLILISHLLEKGLQRLANVCFLLLLLLFLRVFLFKHSL 84

Qy      44 ----------WFQHRHKKALWEALEKMKAELMLVGFISLLLIVTQDPIIAKICISEDAAD 93
                    |   :|| :| |||||:||||||::|||||||    :| | |||:   ||
Db      85 SETYEFVSSQWLWKKHKNSLLEALEKIKAELMILGFISLLL-TFGEPYILKICVPRKAAL 143

Qy      94 VMWPC-KRGT---EGRKPSKYVDY----------CPEGKVALMSTGSLHQLHVFIFVLAV 139
             | ||    |   :   ||    :          | :|   |::   |||||: :| ||:
Db     144 SMLPCLSEDTVLFQKLAPSSLSRHLLAAGDTSINCKQGSEPLITLKGLHQLHILLFFLAI 203

Qy     140 FHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SST 198
           ||: ||:||: |||||:| ||||| || | :|:|: | :| | ||:||||: |    ::|
Db     204 FHIVYSLITMMLSRLKIRGWKKWEQETLSNDYEFSIDHSRLRLTHETSFVREHTSFWTTT 263

Qy     199 PGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGI 258
           |   :|  |||||| || : |||||| |||:|||:   ||:| :|||||:|||||:||||
Db     264 PFFFYVGCFFRQFFVSVERTDYLTLRHGFISAHLAPGRKFNFQRYIKRSLEDDFKLVVGI 323

Qy     259 SLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKG 318
           |  ||   :: |  ::||  || | |  ||:|:| |||||: |:  ||||| :  :|::|
Db     324 SPVLWASFVIFLLFNVNGWRTLFWASIPPLLIILAVGTKLQAIMATMALEIVETHAVVQG 383

Qy     319 APVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMK 378
            |:|: |:::|||  |  :|  ||  |||||||: || |   : ||| |:|    | : |
Db     384 MPLVQGSDRYFWFDCPQLLLHLIHFALFQNAFQITHFFWIWYSFGLKSCFHKDFNLVVSK 443

Qy     379 VVVGLALQFLCSYMTFPLYALVT--------QMGSNMKRSIFDEQTSKALTNWRNTAKEK 430
           : : |    ||||:| |||||||         ||||:||:::|||| :|||  |    | |
Db     444 LFLCLGALILCSYITLPLYALVTQMMKWCVEQMGSHMKKAVFDEQMAKALKKWHKDIKLK 503

Qy     431 K 431
           |
Db     504 K 504


RESULT   7
YML2_ARATH
ID   YML2_ARATH     STANDARD;      PRT;   560 AA.
AC   O22757;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Hypothetical MLO-like protein At2g17480.
GN   AT2G17480 OR MJB20.4 OR F5J6.23.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AC002329; AAB86524.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     12     32       POTENTIAL.
FT   TRANSMEM     47     67       POTENTIAL.
FT   TRANSMEM     93    113       POTENTIAL.
FT   TRANSMEM    182    202       POTENTIAL.
FT   TRANSMEM    305    325       POTENTIAL.
FT   TRANSMEM    397    417       POTENTIAL.
SQ   SEQUENCE   560 AA;  63247 MW;  EAAA9CF15AA6AF49 CRC64;
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  Query Match             37.3%;  Score 1039;  DB 1;  Length 560;
  Best Local Similarity   41.6%;  Pred. No. 8.7e-80;
  Matches  239;  Conservative   85;  Mismatches  145;  Indels  106;  Gaps   16;

Qy       3 DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62
           |:| |  ::| :||:|||| |    ::||||:|  |||:|     ||| || :||||:|| 
Db      32 DEKKVVHKQLNQTPTWAVAAVCTFFIVVSVLLEKLLHKVGKVLWDRHKTALLDALEKIKA 91

Qy      63 ELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPC----------KRGTEGRK------ 106
           |||::|||||||   |  |:  |||    |  | ||            |   |:      
Db      92 ELMVLGFISLLLTFGQTYIL-DICIPSHVARTMLPCPAPNLKKEDDDNGESHRRLLSFEH 150

Qy     107 ---------PSKYVDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKM 156
                  |:|    |  || | |:|  :|||||: || ||:||| || :|: | |||: 
Db     151 RFLSGGEASPTK----CTKEGYVELISAEALHQLHILIFFLAIFHVLYSFLTMMLGRLKI 206

Qy     157 RTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRWVVAFFRQFFRSV 215
           | || || ||:|  |:|: | :||| ||:|||||: |    :  |   :|  ||||||||| 
Db     207 RGWKHWENETSSHNYEFSTDTSRFRLTHETSFVRAHTSFWTRIPFFFYVGCFFRQFFRSV 266

Qy     216 TKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDIN 275
           : |||||| ||| ||:  |:|:| |||||||:|||||||||:
Db     267 GRTDYLTLRNGFIAVHLAPGSQFNFQKYIKRSLEDDFKVVVGMMF--------------- 311

Qy     276 GVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPD 335
           :||      ||::|:| |||||: |:  ||| | || :|:::| |:|: ::::||| ||
Db     312 -IGTA-----IPVIIILAVGTKLQAIMTRMALGITDRHAVVQGMPLVQGNDEYFWFGRPH 365

Qy     336 WVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFP 395
           :|  :|  ||| :|        |   |||    ::::|| : | :  ||||:| |
Db     366 LILHLMHFALFQYSF-----------GSDSCYHPNFKIALVKVAIALGVLCLCSYITLP 413

Qy     396 LYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSP 455
           |||||||||| ||:|:|||||||||  ||   |:|| |: |   :    || : |  :|
Db     414 LYALVTQMGSRMKKSVFDEQTSKALKKWRMAVKKKKGVKATTKRLG---GDGSASPTAST 470

Qy     456 MPSRGS---------SPVHLLHKGMGRSDDPQSA----------PTSPRTQQEARDMYP 495
           : |  |          :|  : ::|:    ||:::          | || :       :
Db     471 VRSTSSVRSLQRYKTTPHSMRYEGL----DPETSDLDTDNEALTPPKSPPS-------FE 519

Qy     496 VVVAHPVHRLNPNDRRRSASSSALEADIPSADFSF 530
           :||     :: ||      :|   | |  | :|||
Db     520 LVV-----KVEPNKTNTGETSRDTETD--SKEFSF 547


RESULT   8
MLO1_ARATH
ID   MLO1_ARATH     STANDARD;      PRT;   526 AA.
AC   O49621; O22766;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   MLO-like protein 1 (AtMlo1) (MLO protein homolog 1) (AtMLO-H1).
GN   MLO1 OR MLO-H1 OR AT4G02600 OR T10P11.12.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Panstruga R.;
RL   Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083488; PubMed=10617198;
RA   Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
RA   Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,
RA   Harris B., Ansorge W., Brandt P., Grivell L.A., Rieger M.,
RA   Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
RA   Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheini T.,
RA   Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA   Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,
RA   Langham S.-A., McCullagh B., Bilham L., Robben J.,
RA   Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
RA   Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA   Weitzenegger T., Bothe G., Ramsperger U., Hilbert H., Braun M.,
RA   Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,
RA   Mooijman P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,
RA   Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,
RA   De Keyser A., Buysshaert C., Gielen J., Villarroel R., De Clercq R.,
RA   Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA   Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,
RA   Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
RA   Borkova D., Bloecker H., Scharfe M., Grimm M., Loehnert T.-H.,
RA   Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
RA   Gabel C., Fuchs M., Fartmann B., Granderath K., Dauner D., Herzl A.,
RA   Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,
RA   Massenet O., Quigley F., Clabauld G., Muendlein A., Felber R.,
RA   Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
RA   Chefdor F., Cooke R., Berger C., Monfort A., Casacuberta E.,
RA   Gibbons T., Weber N., Vandenbol M., Bargues M., Terol J., Torres A.,
RA   Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA   Heijnen L., Schwarz S., Scholler P., Heber S., Francs P., Bielke C.,
RA   Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA   Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
RA   Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,
RA   Sekhon M., Murray J., Sheet P., Cordes M., Abu-Threideh J.,
RA   Stoneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
RA   Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA   Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA   Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
RA   Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
RA   Du H., Ali J., Berghoff A., Jones K., Drone K., Cotton M., Joshu C.,
RA   Antonoiu B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
RA   Ma P., Zhong J., Preston R., Vil D., Shekher M., Matero A., Shah R.,
RA   Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Till S.,
RA   Granat S., Shohdy N., Hasegawa A., Hameed A., Lodhi M., Johnson A.,
RA   Chen E., Marra M., Martienssen R., McCombie W.R.;
RT   "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:769-777(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z95352; CAB08605.1; -.
DR   EMBL; AC002330; AAC78258.1; ALT_SEQ.
DR   EMBL; AL161494; CAB80753.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane; Multigene family.
FT   TRANSMEM     12     32       POTENTIAL.
FT   TRANSMEM     62     82       POTENTIAL.
FT   TRANSMEM    161    181       POTENTIAL.
FT   TRANSMEM    288    308       POTENTIAL.
FT   TRANSMEM    309    329       POTENTIAL.
FT   TRANSMEM    373    393       POTENTIAL.
FT   TRANSMEM    413    433       POTENTIAL.
SQ   SEQUENCE   526 AA;  59126 MW;  8E63C276A71A9768 CRC64;


  Query Match             33.4%;  Score 932.5;  DB 1;  Length 526;
  Best Local Similarity   40.5%;  Pred. No. 7.4e-71;
  Matches  202;  Conservative   79;  Mismatches  167;  Indels   51;  Gaps   10;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
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Db       4 GGEGMSLEFTPTWVVAGVCTVIVAISLAVERLLHYFGTVLKKKKQKPLYEALQKVKEELM 63

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCKR------------------------ 100
Db      64 LLGFISLLLTVFQG-LISKFCVKENVLMHMLPCSLDSRREAGASEHKNVTAKEHFQTFLP 122

Qy     101 --GTEGRKPSKY----VDYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSR 153
Db     123 IVGTTRRLLAEHAAVQVGYCSEKGKVPLLSLEALHHLHIFIFVLAISHVTFCVLTVIFGS 182

Qy     154 LKMRTWKKWETETTSLEYQFANDP------ARFRFTHQTSFVKRH-LGLSSTPGI-RWVV 205
Db     183 TRIHQWKKWEDSIADEKF----DPETALRKRRVTHVHNHAFIKEHFLGIGKDSVILGWTQ 238

Qy     206 AFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGV 265
Db     239 SFLKQFYDSVTKSDYVTLRLGFIMTHCKGNPKLNFHKYMMRALEDDFKQVVGISWYLWIF 298

Qy     266 AILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPS 325
Db     299 VVIFLLLNVNGWHTYFWIAFIPFALLLAVGTKLEHVIAQLAHEVAEKHVAIEGDLVVKPS 358

Qy     326 NKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLAL 385
Db     359 DEHFWFSKPQIVLYLIHFILFQNAFEIAFFFWIWVTYGFDSCIMGQVRYIVPRLVIGVFI 418

Qy     386 QFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIG 445
Db     419 QVLCSYSTLPLYAIVSQMGSSFKKAIFEENVQVGLVGWAQKVKQKR-----DLKAAASNG 473

Qy     446 DATPSR-GSSPMPSRGSSP 463
Db     474 DEGSSQAGPGPDSGSGSAP 492
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RESULT   9
ML15_ARATH
ID   ML15_ARATH     STANDARD;      PRT;   496 AA.
AC   O80580;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   MLO-like protein 15 (AtMlo15).
GN   MLO15 OR AT2G44110 OR F6E13.24.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Devoto A., Hartmann H.A., Piffanelli P., Elliott C., Simmons C.,
RA   Taramino G., Goh C., Cohen F.E., Schulze-Lefert P., Panstruga R.;
RT   "Molecular phylogeny and domain-specific co-evolution of the
RT   plant-specific seven transmembrane MLO family.";
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. COLUMBIA;
RX   MEDLINE=20083487; PubMed=10617197;
RA   Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA   Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA   Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA   Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,
RA   Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA   Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA   Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA   Venter J.C.;
RT   "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 402:761-768(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF369576; AAK53808.1; -.
DR   EMBL; AC004005; AAC23431.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane; Multigene family.
FT   TRANSMEM     10     30       POTENTIAL.
FT   TRANSMEM    270    290       POTENTIAL.
FT   TRANSMEM    398    418       POTENTIAL.
SQ   SEQUENCE   496 AA;  56151 MW;  1B5FBE2DD33DFC3C CRC64;
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  Query Match             33.2%;  Score 927;  DB 1;  Length 496;
  Best Local Similarity   39.9%;  Pred. No. 2e-70;
  Matches  205;  Conservative   89;  Mismatches  168;  Indels   52;  Gaps   11;

Qy      12 LPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGFIS 71
Db       8 LEYTPTWVVALVCSVIVSISFAVERLIHRAGKHFKNNDQKQLFGALQKIKEELMLVGFIS 67

Qy      72 LLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK--------------------YV 111
Db      68 LLLSVGQSK-IAKICISKELSEKFLPCTKPAGAEKSLKDSSHFQFSFTGRHLLAGDAPAG 126

Qy     112 DYCP-EGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLE 170
Db     127 DYCSLKGKVPIMSLSALHELHIFIFVLAVAHIIFCLLTIVFGTMKIKQWKKWEDKV--LE 184

Qy     171 YQFANDPARFRFTH--QTSFVK-RHLGL-SSTPGIRWVVAFFRQFFRSVTKVDYLTLRAG 226
Db     185 KDFDTDQSIKKFTHVQEHEFIRSRFLGVGKADASLGWVQSFMKQFLASVNESDYITMRLG 244

Qy     227 FINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFI 286
Db     245 FVTTHCKTNPKFNFHKYLMRALNSDFKKVVGISWYLWVFVVLFLLLNIVAWHVYFWLAFI 304

Qy     287 PLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLF 346
Db     305 PLILLLAVGTKLEHIITDLAHEVAEKHIAVEGDLVVRPSDDLFWFQSPRLVLFLIHFILF 364

Qy     347 QNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSN 406
Db     365 QNSFEIAYFFFILFQFGWDSCIMDHVKFVIPRLVIGVIIQLLCSYSTLPLYALVTQMGSS 424

Qy     407 MKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHL 466
Db     425 FKGAIFNEQTQEHLVGWAKMAKRGVKKGATQVGTSH---DATSPRPSIQLNS-------L 474

Qy     467 LHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAH 500
Db     475 LGKGSSQQNQ------NPKEKSE--------IAH 494
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RESULT  10
YML3_ARATH
ID   YML3_ARATH     STANDARD;      PRT;   447 AA.
AC   O23693;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   01-MAR-2002 (Rel. 41, Last annotation update)
DE   Hypothetical MLO-like protein At1g11000.
GN   AT1G11000 OR T19D16.26.
OS   Arabidopsis thaliana (Mouse-ear cress).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX   NCBI_TaxID=3702;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. Columbia;
RX   MEDLINE=21016719; PubMed=11130712;
RA   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA   White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA   Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA   Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA   Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA   Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA   Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA   Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA   Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA   Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
RA   Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA   Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA   Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA   Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA   Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA   Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT   "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT   thaliana.";
RL   Nature 408:816-820(2000).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U95973; AAB65495.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Hypothetical protein; Transmembrane.
FT   TRANSMEM     14     34       POTENTIAL.
FT   TRANSMEM     94    114       POTENTIAL.
FT   TRANSMEM    163    183       POTENTIAL.
FT   TRANSMEM    185    205       POTENTIAL.
FT   TRANSMEM    247    267       POTENTIAL.
FT   TRANSMEM    274    294       POTENTIAL.
SQ   SEQUENCE   447 AA;  50608 MW;  027A1C33AE1B5EEA CRC64;


  Query Match             17.9%;  Score 499.5;  DB 1;  Length 447;
  Best Local Similarity   27.2%;  Pred. No. 1.7e-34;
  Matches  140;  Conservative   72;  Mismatches  159;  Indels  143;  Gaps   13;

Qy       4 KKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAE 63
           |:|   | | |||:::|| |   :| |  |:|  ::: |  :   ||| | |
Db       6 KEG---RSLAETPTYSVASVVTVLVFVCFLVERAIYRFGKDY-GIHKKVLLEHTSS---- 57

Qy      64 LMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVALMS 123
                   |    :    | | :                       |  |:   :|
Db      58 -------------TNQSSLPHHGIHEAS-------------------HQCGHGREPFVS 84

Qy     124 TGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFT 183
             | ||  |:||| : || || | | |:  |:
Db      85 YEGLEQLLRFLFVLGITHVLYSGIAIGLAMSKL--------------------------- 117

Qy     184 HQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKY 243
                                 | |||  |: | ||  || ||:  | :    ::|| |
Db     118 ----------------------CFLRQFRGSIRKSDYFALRLGFLTKH-NLPFTYNFHMY 154

Qy     244 IKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIM 303
           : |:|||:|  :|||| ||| ||: : ::::|:    ||||:| :::: |||||| ::
Db     155 MVRTMEDEFHGIVGISWPLWVYAIVCICINVHGLNMYFWISFVPAILVMLVGTKLEHVVS 214

Qy     304 EMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVL----------FFIHLTLFQNAFQMA 353
           ::|||:::: :       |:| :  ||| :|: :|           |:  | ||||:||
Db     215 KLALEVKEQQTGTSNGAQVKPRDGLFWFGKPEILLRLIQFIIFQMILIYFLLMQNAFEMA 274

Qy     354 HFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFD 413
             |:| :                          | ||| | ||  :||||||  |:::
Db     275 TFIWFL--------------------------FWCSYGTVPLNVIVTQMGSRHKKAVIA 307

Qy     414 EQTSKALTNWRNTAKEKKK-VRDTDMLMAQMIGD------ATPSRGSSPMPSRGSSPVHL 466
           |    :| :|    ||: |  |    |    | :       | || || | |     ::
Db     308 ESVRDSLHSWCKRVKERSKHTRSVCSLDTATIDERDEMTVGTLSRSSS-MTSLNQITINS 366

Qy     467 LHK------GMGRSDDPQSAPTSPRTQQEARDMY 494
           : :          |  ||   || | ::   : |
Db     367 IDQAESIFGAAASSSSPQDGYTS-RVEEYLSETY 399


RESULT  11
MLOL_LINUS
ID   MLOL_LINUS     STANDARD;      PRT;   217 AA.
AC   P81785;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   MLO-like protein (Fragment).
OS   Linum usitatissimum (Flax) (Linseed).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC   eurosids I; Malpighiales; Linaceae; Linum.
OX   NCBI_TaxID=4006;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CV. ANTARES; TISSUE=Cotyledon;
RA   McKay G.J.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE MLO FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AJ005341; CAA06487.1; -.
DR   InterPro; IPR004326; Mlo.
DR   Pfam; PF03094; Mlo; 1.
KW   Transmembrane.
FT   NON_TER       1      1
FT   TRANSMEM     35     55       POTENTIAL.
FT   TRANSMEM     59     79       POTENTIAL.
FT   TRANSMEM    119    139       POTENTIAL.
FT   NON_TER     217    217
SQ   SEQUENCE   217 AA;  24604 MW;  4341CE37FC2E8493 CRC64;


  Query Match             15.4%;  Score 429;  DB 1;  Length 217;
  Best Local Similarity   55.4%;  Pred. No. 5.6e-29;
  Matches   82;  Conservative   23;  Mismatches   41;  Indels    2;  Gaps    1;

Qy     224 RAGFINAHLS--QNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLI 281
             |   | |||:    |:||| ||: ||:|||||||||||  ||  |:| |  : :|    :
Db       5 RYPIIAAHLAPGSESRFDFQKYVNRSLEDDFKVVVGISPILWFFAVLFLLSNTHGWVAYL 64

Qy     282 WISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFI 341
           |: ||||:|:| |||||::|| :: | ||||  |:||||||:| :  ||| ||  ||| |
Db      65 WLPFIPLIIILVVGTKLQVIITQLGLSIQDRGDVVKGAPVVQPGDDLFWFGRPRLVLFLI 124

Qy     342 HLTLFQNAFQMAHFVWTVATPGLKKCYH 369
           |  |||||||:| |:|:|   |:| |:|
```

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Db    125 HFCLFQNAFQLAFFIWSVYEFGIKTCFH 152


RESULT  12
YHGE_ECOLI
ID   YHGE_ECOLI     STANDARD;      PRT;   574 AA.
AC   P45804;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein yhgE.
GN   YHGE OR B3402.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: SOME, TO B.SUBTILIS YRDB.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U18997; AAA58199.1; -.
DR   EMBL; AE000415; AAC76427.1; -.
DR   EcoGene; EG12931; yhgE.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM     12     32       POTENTIAL.
FT   TRANSMEM     39     59       POTENTIAL.
FT   TRANSMEM     66     86       POTENTIAL.
FT   TRANSMEM     99    119       POTENTIAL.
FT   TRANSMEM    142    162       POTENTIAL.
FT   TRANSMEM    178    198       POTENTIAL.
FT   TRANSMEM    214    234       POTENTIAL.
FT   TRANSMEM    248    268       POTENTIAL.
FT   TRANSMEM    286    306       POTENTIAL.
FT   TRANSMEM    320    340       POTENTIAL.
FT   TRANSMEM    353    373       POTENTIAL.
SQ   SEQUENCE   574 AA;  64637 MW;  529E33C38D5BEF59 CRC64;


  Query Match             3.7%;  Score 102.5;  DB 1;  Length 574;
  Best Local Similarity   19.7%;  Pred. No. 0.61;
  Matches   69;  Conservative   53;  Mismatches   89;  Indels  139;  Gaps   16;

Qy    111 VDYCPEGKVALMSTGSLHQLHVFIFVL---------AVFHV----------TYSVIT--- 148
          |:  |  :  :::|| | |  :: :           |: |           :|||:
Db      4 VELSPATRWGMIATGLLQGLVCYLLIAWLSGKNHSWIVYGVPATVAFSSVLLFSVISFKQ 63

Qy    149 ---------IALSRLKMRTWKKWETETTS--------------------------LEYQ 172
                  : :: | |  | ||:|:  :                          :
Db     64 KRLWGWLALVFIATLGMSGWLKWQTDGMNPWRAEKALWDFGCYLLLMAMLLLPWIQQSLR 123

Qy    173 FANDPARFRFTHQTSF--VKRHLGLSSTPGIRWVV-------------AFFRQFFRSVTK 217
          || :|:|: :|: :  |   | :    |: |:|               ||   | :
Db    124 IRNDSSRYRYFYQSVWHNVLILLVIFLANGLTWLVLLLWSELFKLVGITFFNTLFFATDW 183

Qy    218 VDYLTLRAGFINA-----HLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFL 272
            ||||  | : |       :|:   |       |::  | ::    |||  |::|||
Db    184 FIYLTL--GLVTALAVILARTQSRLID-------SIQKLFTLIATGLLPL--VSLLTLMF 232

Qy    273 -------------DINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRAS---- 314
                      |:  | |: ::|            |::|:| :  : | :||
Db    233 IITLPFTGLSAISRHISAAGLLLTLAF-----------LQLILMAIVRDPQ-KASLPWT 279

Qy    315 -----VIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTV 359
               :|| | :| |   |       | |:          ::| : |||
Db    280 GPLRCLIKTALLVAPLYVFV----AAWALW----------LRVAQYGWTV 315


RESULT  13
HSLU_HELPJ
ID   HSLU_HELPJ     STANDARD;      PRT;   443 AA.
AC   Q9ZLW1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   ATP-dependent hsl protease ATP-binding subunit hslU.
GN   HSLU OR JHP0465.
OS   Helicobacter pylori J99 (Campylobacter pylori J99).
OC   Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC   Helicobacter.
OX   NCBI_TaxID=85963;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99120557; PubMed=9923682;
RA   Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
RA   Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
RA   Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
RA   Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
RA   Trust T.J.;
RT   "Genomic sequence comparison of two unrelated isolates of the human
RT   gastric pathogen Helicobacter pylori.";
RL   Nature 397:176-180(1999).
CC   -!- FUNCTION: CHAPERONE SUBUNIT OF A PROTEASOME-LIKE DEGRADATION
CC       COMPLEX (BY SIMILARITY).
CC   -!- SUBUNIT: INTERACTS WITH HSLV (BY SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: BELONGS TO THE CLPX CHAPERONE FAMILY. HSLU SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001480; AAD06034.1; -.
DR   HSSP; P32168; 1DO2.
DR   InterPro; IPR003593; AAA.
DR   InterPro; IPR003959; AAA_subfam.
DR   InterPro; IPR001270; CLP_AB.
DR   Pfam; PF00004; AAA; 1.
DR   PRINTS; PR00300; CLPPROTEASEA.
DR   SMART; SM00382; AAA; 1.
KW   Chaperone; ATP-binding; Complete proteome.
FT   NP_BIND      59     66       ATP (POTENTIAL).
SQ   SEQUENCE   443 AA;  50164 MW;  6AF0F90849B686DA CRC64;


  Query Match             3.4%;  Score 95.5;  DB 1;  Length 443;
  Best Local Similarity   22.2%;  Pred. No. 1.7;
  Matches   54;  Conservative   35;  Mismatches   95;  Indels   59;  Gaps   12;

Qy     34 MEHGLHKLGHWFQHRHKKAL--WEALEKMKAEL---MLVGFI----------SLLLIVT 77
          ::  | |: |  | : || |   || | :|||:   :| |             | :: :
Db    196 VQENLIKVFHKEQDKVKKTLSVKEAKEALKAEISDTLLDGEAIKMEGLKRAESSGVIFID 255

Qy     78 QDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCP--EGKVALMSTGSLHQLHVFIF 135
          :   | || :|        | | | :       | |  || |     ||:   |:
Db    256 E---IDKIAVSSKEGSRQDPSKEGVQR------DLLPIVEGSVVNTKYGSIKTEHILFI 305
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Qy     136 VLAVFHVT--YSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHL 193
           ||::    :|     |  :|   : |  |  : |             :|| :|::
Db     306 AAGAFHLSKPSDLIPELQGRFPLRV--ELENLTEEIMYMILTQT-------KTSIIKQYQ 356

Qy     194 GLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFD------FHKYIKRS 247
           |    |:   :||     : : |: |            : | | :       |  |::
Db     357 ALLKVEGVE--IAFEDDAIKELAKLSY-----------NANQKSEDIGARRLHTTIEKV 402

Qy     248 MED 250
           :||
Db     403 LED 405


RESULT  14
NFIC_PIG
ID   NFIC_PIG       STANDARD;      PRT;   506 AA.
AC   P21999;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Nuclear factor 1 C-type (Nuclear factor 1/C) (NF1-C) (NFI-C) (NF-I/C)
DE   (CCAAT-box binding transcription factor) (CTF) (TGGCA-binding
DE   protein).
GN   NFIC OR NFI.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=90105327; PubMed=2513876;
RA   Meisterernst M., Rogge L., Foeckler R., Karaghiosoff M.,
RA   Winnacker E.L.;
RT   "Structural and functional organization of a porcine gene coding for
RT   nuclear factor I.";
RL   Biochemistry 28:8191-8200(1989).
CC   -!- FUNCTION: RECOGNIZES AND BINDS THE PALINDROMIC SEQUENCE 5'-
CC       TTGGCNNNNNGCCAA-3' PRESENT IN VIRAL AND CELLULAR PROMOTERS AND IN
CC       THE ORIGIN OF REPLICATION OF ADENOVIRUS TYPE 2. THESE PROTEINS ARE
CC       INDIVIDUALLY CAPABLE OF ACTIVATING TRANSCRIPTION AND REPLICATION.
CC   -!- SUBUNIT: BINDS DNA AS AN HOMODIMER.
CC   -!- SUBCELLULAR LOCATION: Nuclear.
CC   -!- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS ARE PRODUCED BY
CC       ALTERNATIVE SPLICING.
CC   -!- SIMILARITY: BELONGS TO THE CTF/NF-I FAMILY.
CC   -!- SIMILARITY: CONTAINS 1 DWA/MH1 DOMAIN.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; J02875; AAA31093.1; -.
DR   PIR; A33416; A33416.
DR   TRANSFAC; T00175; -.
DR   TRANSFAC; T00538; -.
DR   InterPro; IPR000647; CTF_NFI.
DR   InterPro; IPR003619; Dwarfin_A.
DR   Pfam; PF00859; CTF_NFI; 1.
DR   SMART; SM00523; DWA; 1.
DR   PROSITE; PS00349; CTF_NFI; 1.
KW   Transcription regulation; DNA replication; DNA-binding; Activator;
KW   Nuclear protein; Multigene family; Alternative splicing.
FT   DOMAIN       68    176       DWA.
SQ   SEQUENCE   506 AA;  55461 MW;  6315A9474807F4C0 CRC64;


  Query Match             3.4%;  Score 95.5;  DB 1;  Length 506;
  Best Local Similarity   23.7%;  Pred. No. 2;
  Matches   66;  Conservative   38;  Mismatches  102;  Indels   73;  Gaps   15;

Qy     291 LLCV-----GTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTL 345
           :|||     |  :: : : :|  :::| :   |:|     :      : |     :  |
Db     161 VLCVQPHHIGVAVKELDLYLAYFVRERDAEQSGSPRAGMGS-----DQEDSKPITLDTTD 215

Qy     346 FQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQF----LCSYMTFPLYALVT 401
           || :| :   |::|           | :|   || |    |    | :| : |    |
Db     216 FQESF-VTSGVFSVT---------ELIQVSRTPVVTGTGPNFSLGELQGHMAYDLNPAST 265

Qy     402 QM----------GSNMKRS-------------IFDEQTSKALTNWRNTAKE-----KKK 432
           |          ||   :|             :   :|   :| || ::
Db     266 GMRRTLPSTSSSGSKRHKSGSMEEDVDTSPGGDYYTSPSSPTSSN-RNWTEDMEGGISSP 324

Qy     433 VRDTDMLMAQMIGDATPSRGSSPMPS-RGSS------PVHLLHKGMGRSDDPQSA---PT 482
           |: |:|       | :|    ||  | | ||      ||  :| |: ||  | ||   ||
Db     325 VKKTEM-------DKSPFNSPSPQDSPRLSSFTQHHRPVIAVHSGIARSPHPSSALHFPT 377

Qy     483 SPRTQQEARDMYP-VVVAHPVHRLNPNDRRRSASSSALE 520
           :   | |   :|   : :| | ||| |  :   | | :
Db     378 TSILPQTASTYFPHTAIRYPPH-LNPQDPLKDLVSLACD 415


RESULT  15
YD49_THEMA
ID   YD49_THEMA     STANDARD;      PRT;   338 AA.
AC   Q9X170;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein TM1349.
GN   TM1349.
OS   Thermotoga maritima.
OC   Bacteria; Thermotogales; Thermotoga.
OX   NCBI_TaxID=2336;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MSB8 / DSM 3109;
RX   MEDLINE=99287316; PubMed=10360571;
RA   Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
RA   Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
RA   McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
RA   Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
RA   Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
RA   Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
RT   "Evidence for lateral gene transfer between Archaea and Bacteria from
RT   genome sequence of Thermotoga maritima.";
RL   Nature 399:323-329(1999).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC   -!- SIMILARITY: BELONGS TO THE UPF0118 (PERM) FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001789; AAD36420.1; -.
DR   TIGR; TM1349; -.
DR   InterPro; IPR002549; UPF0118.
DR   Pfam; PF01594; UPF0118; 1.
KW   Hypothetical protein; Transmembrane; Complete proteome.
FT   TRANSMEM     20     40       POTENTIAL.
FT   TRANSMEM     68     88       POTENTIAL.
FT   TRANSMEM    147    167       POTENTIAL.
FT   TRANSMEM    203    223       POTENTIAL.
FT   TRANSMEM    239    259       POTENTIAL.
FT   TRANSMEM    263    283       POTENTIAL.
FT   TRANSMEM    297    317       POTENTIAL.
SQ   SEQUENCE   338 AA;  39386 MW;  9B21A19682078ADD CRC64;
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  Query Match             3.4%;  Score 94.5;  DB 1;  Length 338;
  Best Local Similarity   23.1%;  Pred. No. 1.4;
  Matches   75;  Conservative   36;  Mismatches   88;  Indels  125;  Gaps   16;

Qy      62 AELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVAL 121
           | ::|: | :|||    ||:|                 |  |  |  ||       :||
Db      35 AVIVLMVFFTLLL----DPVI----------------RFLEKLKFGKYF-----SRVA- 67

Qy     122 MSTGSLHQLHVFIFVLA---------VFHVTYSVITIALSRLKMRTWKKW---------- 162
                  | :| ||:          ||:   | |       : : || :
Db      68 -------ALLLFFFVMVYSLYMIIPPVFNEFGSFIEFMTKVFESKIWKDYIKSPELMPVF 120

Qy     163 -------ETETTS-LEYQFANDPARFRFTHQTSFVKRHLGLSSTP-GIRWVVAFF----- 208
                  | : |  | | |:     |  :  |  |    ||  |   || : :||
Db     121 DKIMNFLEPKLTDFLNYVFSLVTTNF-VSVTTIIVFTLFGLGYTVFYIREIASFFVLIYP 179

Qy     209 -------RQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGIS-- 259
                  |:||| |       :|  ||||                        |::|:|
Db     180 KSVRAEAREFFRDVYASMGRYIRVIFINA----------------------VIIGLSYW 216

Qy     260 ------------LPLWGVAILTLFLDINGVGTLIWISFIPLVIL-LCVGTKLEMIIMEM 305
                       : ||  | :| |: | ||     : :||:::  | :| |  ::|
Db     217 IVFEAFNLKYSAIISLW--AFVTNFIPIVGV----VLEYIPVLLFSLTLGVKGVLLIALF 270

Qy     306 ALEIQDRASVI-----KGAPVVEP 324
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Db     271 AILIHAVAFVVFIQLMKGLEKLNP 294


Search completed: July 23, 2002, 14:33:42
Job time: 497 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 23, 2002, 13:30:27 ; Search time 24.92 Seconds
(without alignments)
522.425 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSSALEADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2788	100.0	533	4	US-09-350-268-3	Sequence 3, Appli
2	1257	45.1	515	4	US-09-183-959-10	Sequence 10, Appl
3	888.5	31.9	492	4	US-09-183-959-2	Sequence 2, Appli
4	801.5	28.7	496	4	US-09-350-268-2	Sequence 2, Appli
5	752.5	27.0	264	4	US-09-183-959-12	Sequence 12, Appl
6	730.5	26.2	509	4	US-09-183-959-8	Sequence 8, Appli
7	478	17.1	114	4	US-09-183-959-14	Sequence 14, Appl
8	193	6.9	80	4	US-09-183-959-4	Sequence 4, Appli
9	129	4.6	52	4	US-09-183-959-6	Sequence 6, Appli
10	93.5	3.4	339	4	US-09-323-873A-2	Sequence 2, Appli
11	90.5	3.2	2787	4	US-09-245-041-15	Sequence 15, Appl
12	89.5	3.2	3079	5	PCT-US94-00198-4	Sequence 4, Appli
13	88	3.2	652	1	US-08-050-684-2	Sequence 2, Appli
14	88	3.2	652	1	US-08-582-719-2	Sequence 2, Appli
15	87	3.1	1835	4	US-09-404-650-5	Sequence 5, Appli
16	85	3.0	364	2	US-08-458-970A-10	Sequence 10, Appl
17	85	3.0	630	4	US-09-300-909-20	Sequence 20, Appl
18	82.5	3.0	765	4	US-08-444-818-70	Sequence 70, Appl
19	81.5	2.9	773	2	US-08-484-101B-42	Sequence 42, Appl
20	81.5	2.9	773	2	US-08-484-101B-44	Sequence 44, Appl
21	81.5	2.9	773	4	US-08-714-524D-42	Sequence 42, Appl
22	81.5	2.9	773	4	US-08-714-524D-44	Sequence 44, Appl
23	80	2.9	1956	4	US-08-843-417-2	Sequence 2, Appli
24	78	2.8	581	4	US-09-331-581-2	Sequence 2, Appli
25	77.5	2.8	465	3	US-08-788-231A-2	Sequence 2, Appli
26	77.5	2.8	524	2	US-08-928-692-12	Sequence 12, Appl
27	77	2.8	2175	4	US-09-404-650-2	Sequence 2, Appli
28	77	2.8	2188	4	US-09-404-650-4	Sequence 4, Appli
29	76.5	2.7	350	1	US-08-118-270-41	Sequence 41, Appl
30	76.5	2.7	350	5	PCT-US93-08528-41	Sequence 41, Appl
31	76.5	2.7	473	1	US-08-439-131A-4	Sequence 4, Appli
32	76.5	2.7	473	1	US-08-440-674-3	Sequence 3, Appli
33	76.5	2.7	663	4	US-08-959-004-5	Sequence 5, Appli
34	76.5	2.7	1440	4	US-09-357-251-37	Sequence 37, Appl
35	76	2.7	318	1	US-08-309-182B-3	Sequence 3, Appli
36	75.5	2.7	782	4	US-08-669-286-10	Sequence 10, Appl
37	75.5	2.7	782	4	US-09-469-253-10	Sequence 10, Appl
38	75.5	2.7	782	4	US-09-642-146-10	Sequence 10, Appl
39	75.5	2.7	2353	4	US-08-984-709A-50	Sequence 50, Appl
40	75	2.7	407	2	US-08-742-440A-3	Sequence 3, Appli
41	75	2.7	430	1	US-08-601-435-2	Sequence 2, Appli
42	75	2.7	430	2	US-08-931-047-2	Sequence 2, Appli
43	75	2.7	430	2	US-08-783-202-2	Sequence 2, Appli
44	75	2.7	601	2	US-08-795-868-16	Sequence 16, Appl
45	75	2.7	602	4	US-09-303-069-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-09-350-268-3
; Sequence 3, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
; TITLE OF INVENTION: in Plants
; FILE REFERENCE: 5718-42A-- Mlo3
; CURRENT APPLICATION NUMBER: US/09/350,268
; CURRENT FILING DATE: 1999-07-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Hordeum vulgare
US-09-350-268-3

Query Match 100.0%; Score 2788; DB 4; Length 533;
Best Local Similarity 100.0%; Pred. No. 2.9e-294;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120

Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
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Db    361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420

Qy    421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480

Qy    481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
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Db    481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533


RESULT   2
US-09-183-959-10
; Sequence 10, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 10
;   LENGTH: 515
;   TYPE: PRT
;   ORGANISM: Zea mays
US-09-183-959-10


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Qy      6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
          |  :||| :||:|||| |   :||:|:|:| ||| :| :| || ||||: |||||:|||||
Db      7 GGNSRELDQTPTWAVASVCGVIVLISILLEKGLHHVGEFFSHRKKKAMVEALEKVKAELM 66

Qy     66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK-----------RGTE----------- 103
          ::|||||||:  |: || |:|||  ||: | |||           | |
Db     67 VLGFISLLLVFGQNYII-KVCISNHAANTMLPCKLEAAAVEGKDGHGKEAAAVVAGKKKV 125

Qy    104 -----GRKPSK----------YVDY-------------------CPEGKVALMSTGSLH 128
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Db    126 AVAVPGKKKKKAAAAADHLGGVVDWPPPYYAHNARMLAEASMATKCPEGKVPLISINALH 185

Qy    129 QLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSF 188
          |||:||| |||||||:|| ||:|| | |:| ||:|| |    :|:|::|| |||||||:|||
Db    186 QLHIFIFFLAVFHVSYSAITMALGRAKIRAWKEWEKEAAGQDYEFSHDPTRFRFTHETSF 245

Qy    189 VKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRS 247
          |::|:  |:  |   ::  |||||||||| : ||  ||  |:| ||:  ||||| ||||||
Db    246 VRQHMNVLNKFPASFYISNFFRQFFRSVRQADYCALRHSFVNVHLAPGSKFDFQKYIKRS 305

Qy    248 MEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMAL 307
          :||||||:|||| |||  |:: |||::||  |::||| :|:||:| |||||: ||  ||:
Db    306 LEDDFKVIVGISPPLWASALIFLFLNVNGWHTMLWISIMPVVIILSVGTKLQGIICRMAI 365

Qy    308 EIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKC 367
          :| :| :|||:| |:|: |: :||| || :||| || |||||  ||: :|:|  :   |:  |
Db    366 DITERHAVIQGIPMVQVSDSYFWFARPTFVLFLIHFTLFQNGFQIIYFLWILYEYGMDSC 425

Qy    368 YHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTA 427
          ::        :: :|: :| ||||:| ||||||:|||| ||:||||||||||| |||  | .
Db    426 FNDSEEFVFARLCLGVVVQVLCSYVTLPLYALVSQMGSTMKQSIFDEQTSKALKNWRAGA 485

Qy    428 KEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS 462
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Db    486 KKKAPTGG-----SKHGGGGSPTAGGSPTKADGDA 515


RESULT   3
US-09-183-959-2
; Sequence 2, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 2
;   LENGTH: 492
;   TYPE: PRT
;   ORGANISM: Zea mays
US-09-183-959-2


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  Best Local Similarity   38.9%;  Pred. No. 7.7e-88;
  Matches  187;  Conservative   96;  Mismatches  157;  Indels   41;  Gaps    8;

Qy      9 ARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVG 68
            |  |  ||:| || | : :||:|:: |  || ||   : :::| |:||| |:| ||||:|
Db      7 AAALEFTPTWIVAAVCSLIVLLSLVAERCLHYLGKTLKRKNQKPLFEALLKVKEELMLLG 66

Qy     69 FISLLLIVTQDPIIAKICISEDAADVMWPCKR--------------GTEGR-------K 106
          |||||| | |  :| : || |     | ||::               || ||       :
Db     67 FISLLLTVFQG-MIRRTCIPERWTFHMLPCEKPDEKAGEAATMEHFVGTLGRIGRRLLQE 125

Qy    107 PSKYVDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETE 165
            :   : |  :||| |:|  ::|||||:|||||: || :|| |: |   ::  {{:{{
Db    126 GTAGAEQCQKKGKVPLLSLEAIHQLHIFIFVLAITHVIFSVTTMLLGGAQIHQWKQWE-- 183

Qy    166 TTSLEYQFANDPARFRFTHQTSFVKRH---LGLSSTPGIRWVVAFFRQFFRSVTKVDYLT 222
            ::     :  :    |   |:|:    :|  |   : |: :| :||:|||:| || |
Db    184 -NGIKKDAPGNGPKVTNVHHHEFIKKRFKGIGKDSII-LSWLHSFGKQFYRSVSKSDYTT 241

Qy    223 LRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIW 282
          :| |||  |   | ||||||:|: | :| {{{ {{{{{  {{   :: | |::{{  |  |
Db    242 MRLGFIMTHCPGNPKFDFHRYMVRVLEADFKKVVGISWYLWVFVVIFLLLNVNGWHTYFW 301

Qy    283 ISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIH 342
          |:|:||::|| :||||| :| ::| :: :: : ::|  :|:||:: ||| :|  :|: ||
Db    302 IAFLPLILLLAIGTKLEHVIAQLAHDVAEKHTAVEGDVIVKPSDEHFWFGKPRVILYLIH 361

Qy    343 LTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQ 402
            {{{{::| | | ::| |   |   |:   : ::|:|: :| |||| | ||||:|||
Db    362 FILFQNAFEIAFFFWILSTYGFDSCIMGQVRFIVPRLVIGVVIQLLCSYSTLPLYAIVTQ 421

Qy    403 MGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS 462
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Db    422 MGSCYKKEIFNEHVQQGVLGWAQKVKMKKGLK----------GAASASKDESITNADSAG 471

Qy    463 P 463
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Db    472 P 472


RESULT   4
US-09-350-268-2
; Sequence 2, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
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;  APPLICANT: Simmons, Carl R.
;  TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
;  TITLE OF INVENTION: in Plants
;  FILE REFERENCE: 5718-42A-- Mlo3
;  CURRENT APPLICATION NUMBER: US/09/350,268
;  CURRENT FILING DATE: 1999-07-06
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 496
;   TYPE: PRT
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Mlo3
US-09-350-268-2


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  Matches  182;  Conservative   92;  Mismatches  183;  Indels   45;  Gaps   13;

Qy      12 LPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGFIS 71
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Qy      72 LLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKY---------------------- 110
           |||:|:|| :| |||| :   :   || ||      : |
Db      66 LLLVVSQD-LIQKICIDDSLMEHWMPC-RGASATASAHYGVSSSSSSSAVGGGRRMLKGG 123

Qy     111 ---VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETET 166
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Db     124 GAAFGHCSSKGKVPLLSLHALEQVHIFIFVLAITQVVLSVATVLLGLLQMRIWMHWE--- 180

Qy     167 TSLEYQFANDPARFRFTHQTSFVK-RHLGLSSTPG-IRWVVAFFRQFFRSVTKVDYLTLR 224
            ::: : :: |       :  |:: |  |       | |: :||:||: ||:  ||: :|
Db     181 NTIQQEGSSAPKMIARVQKIRFIQDRCKGYEKAAWVIIWLRSFFKQFYGSVSNDDYIAMR 240

Qy     225 AGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWIS 284
            ||:  |   : ||:|: |: :::| ||| || |    |   :: | |:: |  :  |||
Db     241 LGFVMEHFRGHPKFNFYDYMIKALEKDFKRVVSIKWYYWIFVMIFLLLNVTGWHSYFWIS 300

Qy     285 FIPLVILLCVGTKLEMIIMEMALEIQDR--ASVIKGAPVVEPSNKFFWFHRPDWVLFFIH 342
           :|| :|| :||||| ||  :| |:  :  |   :|  || ||:: |||  |  ||  ||
Db     301 LVPLALLLLIGTKLEHIINRLAYEVASKHAAGQGEGGIVVSPSDELFWFRSPRLVLVLIH 360

Qy     343 LTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQ 402
             ||||||: |:| ||:|  |   |    :| |: :::: : :| |||| | ||||:|:
Db     361 FILFQNAFEFAYFFWTLAMFGANSCIMDSLGYSVSRIIICVVVQVLCSYSTLPLYAIVSH 420

Qy     403 MGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIG-DATPSRGSSPMPSRGS 461
           |||: | ::| :  :  |  | : |: : : |    : |  :|  |  ||       |:
Db     421 MGSSFKSAVFVDDVADNLRGWADGARRRVR-RSATGVDASCLGTPAAAGRG-----WEGA 474

Qy     462 SPVHLLHKGMGRSDDPQSAPTS 483
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Db     475 AGWRLI---AGRPSRPTQQPRS 493


RESULT   5
US-09-183-959-12
; Sequence 12, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 12
;   LENGTH: 264
;   TYPE: PRT
;   ORGANISM: Zea mays
US-09-183-959-12


  Query Match             27.0%;  Score 752.5;  DB 4;  Length 264;
  Best Local Similarity   55.4%;  Pred. No. 1.8e-73;
  Matches  139;  Conservative   49;  Mismatches   62;  Indels    1;  Gaps    1;

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Db       1 RFTHETSFVRQHMNVLNKFPASFYISNFFRQFFRSVRRADYCALRHSFVNVHLAPGTKFD 60

Qy     240 FHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLE 299
           | |||||:||||||:|||| |||  |:: |||::||  |::||| :|:||:| |||||:
Db      61 FQKYIKRSLEDDFKVIVGISPPLWASALIFLFLNVNGWHTMLWISIMPVVIILSVGTKLQ 120

Qy     300 MIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTV 359
            ||  ||::| :| :||:| |:|: |: :||| || :||| || ||||| ||: :|:| :
Db     121 GIICRMAIDITERHAVIQGIPLVQVSDSYFWFARPTFVLFLIHFTLFQNGFQIIYFLWIL 180

Qy     360 ATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKA 419
             |:  |::        :: :|: :| |||:| ||||||:|||| ||:||||||||||
Db     181 YEYGMDSCFNDSEEFVFARLCLGVVVQVLCSYVTLPLYALVSQMGSTMKQSIFDEQTSKA 240

Qy     420 LTNWRNTAKEK 430
           | |||  ||:|
Db     241 LKNWRAGAKKK 251


RESULT   6
US-09-183-959-8
; Sequence 8, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 8
;   LENGTH: 509
;   TYPE: PRT
;   ORGANISM: Zea mays
US-09-183-959-8


  Query Match             26.2%;  Score 730.5;  DB 4;  Length 509;
  Best Local Similarity   33.8%;  Pred. No. 1.2e-70;
  Matches  155;  Conservative  101;  Mismatches  162;  Indels   41;  Gaps   10;

Qy       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
           |: ::|   | | |||:|:|| |   ||    |:|  | :   | :   :||:  ||||:
Db       1 MAAEQG---RSLAETPTWSVATVTTLMVAACFLVERSLSRFAKWLRKTKRKAMLAALEKI 57

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICI------------SEDAADVMWPCKRGTEGRKP 107
           : ||||:| |||||  |    |::||:                |  |::   | |:  :
Db      58 REELMLLGVISLLLSQTA-RFISEICVPSSLFTSRFYICSESDYQDLL----RNTDANQT 112

Qy     108 S--------KYVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTW 159
           :        : :  | ||    :|   | ||| |:|:| : || || :|: || :|: :|
Db     113 ALDKNMFGGQRLHVCGEGHEPFVSYEGLEQLHRFLFILGITHVLYSFVTVVLSMIKIYSW 172
```

```
Qy    160 KKWETETTSLEYQFANDPARFRFT----HQTSFVKRHLG--LSSTPGIRWVVAFFRQFFR 213
          :|||| |  | : : | |  |::|| :  |  : |:: | |||
Db    173 RKWET----LAGPIAAEELKARRTKVMRRQSTFVFNNASHPWSKNKILIWMLCFLRQFKG 228

Qy    214 SVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLD 273
          |: : ||| || ||:  |  :| :|||||: ||||||:  :||| |||  ||: : ::
Db    229 SIIRSDYLALRLGFVTYHKLPHS-YDFHKYMVRSMEDDYNGTIGISWPLWAYAIVCILIN 287

Qy    274 INGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHR 333
          ::|:  |:||:|::::| |||:|: :| ::|||: :  :  |:  ::  :  ||| :
Db    288 VHGINIYFWLSFVPVILVLLVGTELQHVIAQLALEVAEATAPYVGSQ-LKLRDDLFWFGK 346

Qy    334 PDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMT 393
          |  : : |  |||||::| |:|::  : |:  :  :::: || :|| ||| |
Db    347 PRVLWWLIQFISFQNAFELATFLWSLWELSAQTCFMKHYYMVAIRLISGLLVQFWCSYST 406

Qy    394 FPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKK 432
           ||  :::||| |:|:  |  ::| :|  |:: :
Db    407 LPLNVIISQMGPKFKKSLVSENVRESLHSWCKRVKDRSR 445
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RESULT 7
US-09-183-959-14
; Sequence 14, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 14
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-14

Query Match 17.1%; Score 478; DB 4; Length 114;
Best Local Similarity 74.6%; Pred. No. 3.2e-44;
Matches 85; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

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Qy    322 VEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVV 381
          ||||::|||||:|| |||| |||||||||||||||||: || |||||| ::|||||||
Db      1 VEPSDRFFWFNRPGWVLFLIHLTLFQNAFQMAHFVWTLLTPDLKKCYHERLGLSIMKVAV 60

Qy    382 GLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRD 435
          || || ||||:|||||||||||||:||::||:|||:||:  || |||:| : |:
Db     61 GLVLQVLCSYITFPLYALVTQMGSHMKKTIFEEQTAKAVMKWRKTAKDKVRQRE 114
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RESULT 8
US-09-183-959-4
; Sequence 4, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 4
; LENGTH: 80
; TYPE: PRT
; ORGANISM: Zea mays
US-09-183-959-4

Query Match 6.9%; Score 193; DB 4; Length 80;
Best Local Similarity 51.3%; Pred. No. 1.8e-13;
Matches 40; Conservative 11; Mismatches 27; Indels 0; Gaps 0;

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Qy    231 HLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVI 290
          |  :    |||||: |::| :|| |||||  ||   || | |:|||  |  |::|:|| :
Db      1 HYPEKPDIDFHKYMTRAVEYEFKRVVGISWYLWLFVILFLLLNINGWHTYFWLAFLPLFL 60

Qy    291 LLCVGTKLEMIIMEMALE 308
          || || ||| ||  :| |
Db     61 LLIVGAKLEHIITRLAQE 78
```

RESULT 9
US-09-183-959-6
; Sequence 6, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 6
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (4)
US-09-183-959-6

Query Match 4.6%; Score 129; DB 4; Length 52;
Best Local Similarity 46.2%; Pred. No. 8.1e-07;
Matches 24; Conservative 8; Mismatches 20; Indels 0; Gaps 0;

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Qy    383 LALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVR 434
          : :  |||| | ||||:||||||  |: ||:|   : :  |    | || :|
Db      1 VVIXLLCSYSTLPLYAIVTQMGSCYKKEIFNEHVQQGVLGWAQKVKMKKGLR 52
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RESULT 10
US-09-323-873A-2
; Sequence 2, Application US/09323873A
; Patent No. 6329503
; GENERAL INFORMATION:
; APPLICANT: Daniel E. Afar
; APPLICANT: Rene S. Hubert
; APPLICANT: Kahan Leong
; APPLICANT: Arthur B. Raitano
; APPLICANT: Douglas C. Saffran
; APPLICANT: Steve Chappell Mitchell
; TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS
; TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF
; FILE REFERENCE: 129.16USU2

```
;  CURRENT APPLICATION NUMBER: US/09/323,873A
;  CURRENT FILING DATE:  1999-06-01
;  PRIOR APPLICATION NUMBER: 60/087,520
;  PRIOR FILING DATE: 1998-06-01
;  PRIOR APPLICATION NUMBER: 60/091,183
;  PRIOR FILING DATE: 1998-06-30
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
;   LENGTH: 339
;   TYPE: PRT
;   ORGANISM: Homo Sapiens
US-09-323-873A-2


  Query Match             3.4%;  Score 93.5;  DB 4;  Length 339;
  Best Local Similarity   21.7%;  Pred. No. 0.11;
  Matches   68;  Conservative   48;  Mismatches  113;  Indels   85;  Gaps   16;

Qy       2 SDKKGVPARELPET----PSW----AVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKAL 53
           :|:   |: ||  |    | |     :| : |::  :  |:  :| |    |     |
Db      52 ADEFDCPS-ELQHTQELFPQWHLPIKIAAIIASLTFLYTLLREVIHPLATSHQQYFYKIP 110

Qy      54 WEALEKMKAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY 113
             : |:   | :|  |:|| :|    :|| |              ||: :|   ::|
Db     111 ILVINKV---LPMVS-ITLLALVYLPGVIAAIV----------QLHNGTKYKKFPHWLD- 155

Qy     114 CPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALS-------RLKMRTWKKWETET 166
             |  |    :  |  :  |  || |  ||      ||        | |:  |   : :
Db     156 ----KWML----TRKQFGLLSFFFAVLHAIYS-----LSYPMRRSYRYKLLNWAYQQVQQ 202

Qy     167 TSLEYQFANDPARFRFTHQTSFV----KRHLGLSSTPGI----RWVVAFFRQFFRSVTKV 218
             :   :|  |          |       | ::| | :     |     |:|    :|:
Db     203 NKEDAWIEHDVWRMEIYVSLGIVGLAILALLAVTSIPSVSDSLTW-----REFHYIQSKL 257

Qy     219 DYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVG 278
           ::|  | |:| :     | ::|:|      | |  |  : | : :|:
Db     258 GIVSLLLGTIHALI-----FAWNKWI------DIKQFVWYTPPTFMIAV---------- 295

Qy     279 TLIWISFIPLVILL 292
                 |:|:|:|:
Db     296 ------FLPIVVLI 303


RESULT  11
US-09-245-041-15
; Sequence 15, Application US/09245041
; Patent No. 6274339
; GENERAL INFORMATION:
;  APPLICANT: Moore, K.
;  APPLICANT: Nagle, D.
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT
;  TITLE OF INVENTION: OF BODY WEIGHT DISORDERS INCLUDING OBESITY
;  FILE REFERENCE: 7853-136
;  CURRENT APPLICATION NUMBER: US/09/245,041
;  CURRENT FILING DATE: 1999-02-05
;  EARLIER APPLICATION NUMBER: 60/093,630
;  EARLIER FILING DATE: 1998-07-21
;  EARLIER APPLICATION NUMBER: 60/104,978
;  EARLIER FILING DATE: 1998-10-20
;  NUMBER OF SEQ ID NOS: 131
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 15
;   LENGTH: 2787
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-245-041-15


  Query Match             3.2%;  Score 90.5;  DB 4;  Length 2787;
  Best Local Similarity   18.5%;  Pred. No. 6.7;
  Matches   89;  Conservative   64;  Mismatches  190;  Indels  137;  Gaps   20;

Qy      85 ICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTY 144
           ||      ::   |  |||  ||||:: :  : |::|    ::  : |    | : |  |
Db    1447 ICREGRGGEMAVRC--GTEDWKPSKHLTHLHDHKLSL----TVSPIRVPASNLLLLHRKY 1500

Qy     145 SVITI---------ALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL 195
           :: :          :|:    :   |:|  ::           |   | :| |  | ||
Db    1501 LILQVQGADGCWRRPVSQENEHSGSLWKTVLGTVSTVQKTKDGVFTSRHSSSVVLEH-GL 1559

Qy     196 SSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVV 255
             |  :  |       | : |              || |   | | |
Db    1560 LKTSQMNLVFISLLSFLKDVL----------FILARFRQLSLFQ---------------- 1593

Qy     256 VGISLPL---WGVAILTLFLDINGV----------GTLIWISFIPLVILLCVGTKLEMI 301
           |:   |   | ::   : |   |             |: : :  |: |: :  || :
Db    1594 -GVPFFLVENWSISFDHIKLGKGGYFKCQGQQCYFECKLVVVFYSNLINLVLIHLKLSL- 1651

Qy     302 IMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVAT 361
                              |   |            |   :|||      ::|
Db    1652 -----------------PFSLP-----------VPLLLHLTL-----PLSHI------ 1670

Qy     362 PGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALV---TQMGSNMKRSIFDEQTSK 418
                |||      |  :   :|   :  |   | ||     :       ||     |
Db    1671 -------HTQTHTHNTK-CLDFKIQLESAVFTLHSYILVKFKLPLAICFFSKIF--AARK 1720

Qy     419 ALTNWRN--TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMP---------SRGSSPVHLL 467
           :: ||  ::::::|    :: :  ::   | ||   |:|          |     |
Db    1721 EFSHPRNISSSRDERKAEMNELKLLFLLSKRTLSR-RRPLPPPPCHPRPDKRSEERTHSC 1779

Qy     468 HKGMGRSDD------PQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEA 521
           |  : | :          | |   |    |       :| |    :: : |: :||    ||
Db    1780 HASLSRKEHEHLGPLDQRASVCPAASSE-------LVVHSQAGVDSDARKGTASHCQAEA 1832


RESULT  12
PCT-US94-00198-4
; Sequence 4, Application PC/TUS9400198
;  GENERAL INFORMATION:
;    APPLICANT:  Schering Corp.
;    TITLE OF INVENTION:  RAS Associated GAP Proteins
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Schering Corp.
;      STREET:  1 Girald Farms
;      CITY:  Madison
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  94304-1104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  Macintosh
;      OPERATING SYSTEM:  6.0.8
;      SOFTWARE:  Microsoft Word 5.1a
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US94/00198
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/004,824
;      FILING DATE:  15-JAN-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lunn, Paul G.
;      REGISTRATION NUMBER:  32,743
;      REFERENCE/DOCKET NUMBER:  DX0352 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201)822-7255
;      TELEFAX:  (201)822-7039
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  3079 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
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;    ORIGINAL SOURCE:
;      ORGANISM:  Saccharomyces cerevisiae
PCT-US94-00198-4


  Query Match             3.2%;  Score 89.5;  DB 5;  Length 3079;
  Best Local Similarity   18.6%;  Pred. No. 10;
  Matches   95;  Conservative   73;  Mismatches  165;  Indels  179;  Gaps   22;

Qy      90 DAADVMWPCKRGTEGRKPSKYVD-YCPEGKV---------ALMSTGSLHQ---------- 129
           |:  : :|   || ||  : :|  |  : |:          :|  : |:
Db    1190 DSEKLTFPLIMGTVGR--ALFVSLYSSQQKIEKTLKIAYTEYLSAINFHERNIDDADKTW 1247

Qy     130 LHVFIFVLAVFHVTYSVI-TIALSR------LKMRT------------WKKWETET--T 167
           :|   || |: |  |:   :||  |      |:  |            :||| | |
Db    1248 VHNIEFVEAMCHDNYTTSGSIAFQRRTRNNILRFATIPNAILLDSMRMIYKKWHTYTHSK 1307

Qy     168 SLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWV-VAFFRQFFRSVTKVDYLTLRAG 226
           ||| |  ||   |               |:|  || ::     :: :  :  :| ::
Db    1308 SLEKQERNDFRNFAGI----------LASLSGILFINKKILQEMYPYL--LDTVSELKK 1354

Qy     227 FINAHLSQNSKF-DFHKYIKRSMEDDFKVVV----------GISLPLWGVAILTLFLDI 274
           |:: :|:  :: ::   : |    |   |             : | |  :|   | :
Db    1355 NIDSFISKQCQWLNYPDLLTRENSRDILSVELHPLSFNLLFNNLRLKLKELACSDLSIPE 1414

Qy     275 NGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASV----IKGAPVVEPSNKFFW 330
           |    ::    | ::  :       ::|  : || |   :    ||  |
Db    1415 NESSYVLLEQIIKMLRTILGRDDDNYVMMLFSTEIVDLIDLLTDEIKKIPA--------- 1465

Qy     331 FHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCS 390
           : | ::   | :|   :| | :         |:|  :| :
Db    1466 -YCPKYLKAIIQMTKMFSALQHSE-----VNLGVKNHFHVK------------------ 1500

Qy     391 YMTFPLYALVTQMGSNMKRSIFDEQTSKALTNW----------RNTAKEKKKV----RD 435
                              :  : :|:|            | :|  |::    ||
Db    1501 ----------------------NKWLRQITDWFQVSIAREYDFENLSKPLKEMDLVKRD 1537

Qy     436 TDMLMAQMIGDAT-------------PSRGSSPMPSRGSSPV-----HLLHKGMGRSDD 476
           |:|      :|:              |   | |  ||  | :     ::| ||: :| |
Db    1538 MDILYIDTAIEASTAIAYLTRHTFLEIPPAASDPELSRSRSVIFGFYFNILMKGLEKSSD 1597

Qy     477 PQSAPTSPRTQQEARDMYPVVVAHPVHRLNPN 508
                       || ||| : | :  || |
Db    1598 -------------RDNYPVFLRHKMSVLNDN 1615


RESULT  13
US-08-050-684-2
; Sequence 2, Application US/08050684
; Patent No. 5550221
;  GENERAL INFORMATION:
;    APPLICANT:  Johann Dr., Stephen V.
;    APPLICANT:  Van Zeijl Dr., Marja
;    APPLICANT:  O'Hara Dr., Bryan M.
;    TITLE OF INVENTION:  Amphotropic Virus Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  American Cyanamid Company
;      STREET:  1937 West Main Street
;      CITY:  Stamford
;      STATE:  CT
;      COUNTRY:  United States of America
;      ZIP:  06904-0060
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/050,684
;      FILING DATE:  16-APR-1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lowney Dr., Karen A
;      REGISTRATION NUMBER:  31,274
;      REFERENCE/DOCKET NUMBER:  31937-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  203-321-2361
;      TELEFAX:  203-321-2971
;      TELEX:  710-474-4059
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  652 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-050-684-2


  Query Match             3.2%;  Score 88;  DB 1;  Length 652;
  Best Local Similarity   19.4%;  Pred. No. 1.3;
  Matches   78;  Conservative   41;  Mismatches  120;  Indels  164;  Gaps   16;

Qy     222 TLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDING----V 277
           |:| | |: :|       ::: ::  |  :   :|| :  :| :    | | |:|    |
Db      69 TIRKGIIDVNL-------YNETVETLMAGEVSAMVGSA--VWQLIASFLRLPISGTHCIV 119

Qy     278 GTLIWISFIPLVILLCVGTK----LEMI-------------IMEMALEIQDRASVIK-- 317
           |: |  |      |: :|||    :|::               |   | :  |  ::|
Db     120 GSTIGFS------LVAIGTKGVQWMELVKIVASWFISPLLSGFMSGLLFVLIRIFILKKE 173

Qy     318 ---------------------------GAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNA 349
                                        ||||:          | |    | |  | |
Db     174 DPVPNGLRALPVFYAATIAINVFSIMYTGAPVL-------GLVLPMWA---IALISFGVA 223

Qy     350 FQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKR 409
             | |||                              |:| :|   :   : : |:  :
Db     224 LLFAFFVWL---------------------------FVCPWMRRKITGKLQKEGALSR- 254

Qy     410 SIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP------ 463
             : ||  ||          ||    :  |    : | |  : |:|   | || |
Db     255 -VSDESLSKVQEAESPVFKELPGAKANDDSTIPLTGAAGETLGTSEGTSAGSHPRAAYGR 313

Qy     464 ------------------------------VHLLHKGMGRSDD----------PQSAPTS 483
                                          | :||  |   |          |:  |
Db     314 ALSMTHGSVKSPISNGTFGFDGHTRSDGHVYHTVHKDSGLYKDLLHKIHIDRGPEEKPAQ 373

Qy     484 PRTQQEAR--DMYPVVVAH----PVHRLNPNDRRRSASSSALE 520
             :  |  : |    |     |||        |:| ||| |
Db     374 ESNYRLLRRNNSYTCYTAAICGLPVHA-----TFRAADSSAPE 411


RESULT  14
US-08-582-719-2
; Sequence 2, Application US/08582719
; Patent No. 5633348
;  GENERAL INFORMATION:
;    APPLICANT:  Johann Dr., Stephen V.
;    APPLICANT:  Van Zeijl Dr., Marja
;    APPLICANT:  O'Hara Dr., Bryan M.
;    TITLE OF INVENTION:  Amphotropic Virus Receptor
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  American Cyanamid Company
;      STREET:  1937 West Main Street
;      CITY:  Stamford
;      STATE:  CT
;      COUNTRY:  United States of America
;      ZIP:  06904-0060
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/582,719
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;      FILING DATE:  04-JAN-1996
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/050,684
;      FILING DATE:  16-APR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lowney Dr., Karen A
;      REGISTRATION NUMBER:  31,274
;      REFERENCE/DOCKET NUMBER:  31937-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  203-321-2361
;      TELEFAX:  203-321-2971
;      TELEX:  710-474-4059
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  652 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-582-719-2


  Query Match             3.2%;  Score 88;  DB 1;  Length 652;
  Best Local Similarity   19.4%;  Pred. No. 1.3;
  Matches   78;  Conservative   41;  Mismatches  120;  Indels  164;  Gaps   16;

Qy     222 TLRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDING----V 277
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Db      69 TIRKGIIDVNL-------YNETVETLMAGEVSAMVGSA--VWQLIASFLRLPISGTHCIV 119

Qy     278 GTLIWISFIPLVILLCVGTK----LEMI-------------IMEMALEIQDRASVIK-- 317
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Db     120 GSTIGFS------LVAIGTKGVQWMELVKIVASWFISPLLSGFMSGLLFVLIRIFILKKE 173

Qy     318 ---------------------------GAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNA 349
                                       ||||:           | |    | |  |  |
Db     174 DPVPNGLRALPVFYAATIAINVFSIMYTGAPVL-------GLVLPMWA---IALISFGVA 223

Qy     350 FQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKR 409
             | |||                              |:| :|   :   : : |:  :
Db     224 LLFAFFVWL---------------------------FVCPWMRRKITGKLQKEGALSR- 254

Qy     410 SIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP------ 463
            : ||  ||         ||    :  |     : | |  : |:|   | || |
Db     255 -VSDESLSKVQEAESPVFKELPGAKANDDSTIPLTGAAGETLGTSEGTSAGSHPRAAYGR 313

Qy     464 ----------------------------VHLLHKGMGRSDD----------PQSAPTS 483
                                        | :||  |   |          |:  |
Db     314 ALSMTHGSVKSPISNGTFGFDGHTRSDGHVYHTVHKDSGLYKDLLHKIHIDRGPEEKPAQ 373

Qy     484 PRTQQEAR--DMYPVVVAH----PVHRLNPNDRRRSASSSALE 520
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RESULT  15
US-09-404-650-5
; Sequence 5, Application US/09404650
; Patent No. 6309858
; GENERAL INFORMATION:
;  APPLICANT: Dietrich, Paul S.
;  APPLICANT: McGivern, Joseph G.
;  TITLE OF INVENTION: T-TYPE CALCIUM CHANNEL VARIANTS; COMPOSITIONS THEREOF;
;  TITLE OF INVENTION: AND USES
;  FILE REFERENCE: R0043B-REG sequence listing
;  CURRENT APPLICATION NUMBER: US/09/404,650
;  CURRENT FILING DATE: 1999-09-23
;  NUMBER OF SEQ ID NOS: 12
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1835
;   TYPE: PRT
;   ORGANISM: Rattus sp.
US-09-404-650-5


  Query Match             3.1%;  Score 87;  DB 4;  Length 1835;
  Best Local Similarity   18.8%;  Pred. No. 8.3;
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Qy      65 MLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEG-----------------RK 106
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Db    1366 MLLYFISFLLIVSFFVLNMFVGV---VVENFHKCRQHQEAEEARRREEKRLRRLEKKRRK 1422

Qy     107 PSK---YVDYCPEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWE 163
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Db    1423 AQRLPYYATYCPT-RLLIHSMCTSHYLDIFI----TFIICLNVVTMSLEHYNQPT----- 1472

Qy     164 TETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAF-FRQFFRSVTKVDYLT 222
           :  |:|:|       : ||  | ||           :  :|||  |:||:
Db    1473 SLETALKY------CNYMFT--TVFV--------LEAVLKLVAFGLRRFFKD-------- 1508

Qy     223 LRAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIW 282
                                   |  : |  :|:   | : |: :    ::||
Db    1509 ----------------------RWNQLDLAIVL---LSVMGITLEE--IEINAA----- 1535

Qy     283 ISFIPLVILLCVGTKLEMIIMEMALEIQDRA---SVIKGAPVVEPSNKFFWFHRPDWVLF 339
           :   | :| :    ::  ::  : :    ||   :|::  | |      |       :||
Db    1536 LPINPTIIRIMRVLRIARVLKLLKMATGMRALLDTVVQALPQVGNLGLLF------MLLF 1589

Qy     340 FIHLTL----------------------FQNAFQMAHFVWTVATPG----------LK 365
           ||:  |                      |:| | ||       : |          |:
Db    1590 FIYAALGVELFGKLVCNDENPCEGMSRHATFEN-FGMAFLTLFQVSTGDNWNGIMKDTLR 1648

Qy     366 KCYHTQ-IGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWR 424
           | | :   || :: |  |   :  |::    : |:  : : : : |          :
Db    1649 DCTHDERTCLSSLQFVSPL---YFVSFVLTAQFVLINVVVAVLMKHLDDSN--------K 1697

Qy     425 NTAKEKKKVRDTDMLMAQMIGDA-------------TPSRG-----SSP-MPSRGSSPVH 465
             :: :   : :: ||  :|                 |  |     |||  | |||
Db    1698 EAQEDAEMDAEIELEMAHGLGPCPGPCPGPCPCPCPCPCAGPRLPTSSPGAPGRGSG--- 1754

Qy     466 LLHKGMGRSDDPQS 479
             | |   | :|
Db    1755 ----GAGAGGDTES 1764


Search completed: July 23, 2002, 14:25:22
Job time: 3295 sec
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GenCore version 4.5

OM protein - protein search, using sw model

Run on: July 23, 2002, 13:27:22 ; Search time 61.82 Seconds
(without alignments)
957.657 Million cell updates/sec

Title: US-09-722-377-1
Perfect score: 2788
Sequence: 1 MSDKKGVPARELPETPSWAV.....ASSSALEADIPSADFSFSQG 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:*
22: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2788	100.0	533	19	AAW59442	Hordeum vulgare ML
2	2788	100.0	533	21	AAB03401	Barley Mlo protein
3	2782	99.8	533	19	AAW59443	Hordeum vulgare ML
4	2434	87.3	534	21	AAB01805	Wheat Mlo homologu
5	2433	87.3	534	20	AAY26966	Wheat Mlo fungal r
6	2433	87.3	534	20	AAY26968	Wheat Mlo fungal r
7	2433	87.3	534	22	AAB31250	Amino acid sequenc
8	2433	87.3	534	22	AAB31252	Amino acid sequenc
9	2432	87.2	534	20	AAY26967	Wheat Mlo fungal r
10	2432	87.2	534	22	AAB31251	Amino acid sequenc
11	1927	69.1	544	19	AAW59445	Hordeum vulgare ML
12	1767.5	63.4	536	19	AAW59444	Oryza sativa MLO p
13	1257	45.1	515	20	AAY14139	Zea mays SCLBr pro
14	1257	45.1	515	21	AAY44605	Maize MLO6 protein
15	1253.5	45.0	573	20	AAY26970	Arabidopsis thalia
16	1253.5	45.0	573	21	AAG35698	Arabidopsis thalia
17	1253.5	45.0	573	22	AAB31254	Amino acid sequenc
18	1234.5	44.3	583	21	AAB03404	Arabidopsis thalia
19	1160	41.6	565	21	AAY44602	Maize MLO2 protein
20	1134.5	40.7	569	20	AAY26969	Arabidopsis thalia
21	1134.5	40.7	569	22	AAB31253	Amino acid sequenc
22	1130.5	40.5	593	20	AAY26972	Arabidopsis thalia
23	1130.5	40.5	593	22	AAB31256	Amino acid sequenc
24	1100	39.5	542	21	AAB03402	Arabidopsis thalia
25	1098	39.4	221	21	AAB01797	Wheat Mlo homologu
26	1072	38.5	530	21	AAB01795	Soybean Mlo homolo
27	1071.5	38.4	511	21	AAG35699	Arabidopsis thalia
28	998	35.8	482	21	AAG35700	Arabidopsis thalia
29	944	33.9	506	21	AAB01793	Soybean Mlo homolo
30	932.5	33.4	526	19	AAW59446	Arabidopsis thalia
31	932.5	33.4	526	21	AAB03403	Arabidopsis thalia
32	927.5	33.3	526	22	AAB31255	Amino acid sequenc
33	924.5	33.2	526	20	AAY26971	Arabidopsis thalia
34	916	32.9	187	21	AAB01794	Soybean Mlo homolo
35	888.5	31.9	492	20	AAY14135	Zea mays SCLBr pro
36	888.5	31.9	492	21	AAY44607	Maize MLO8 protein
37	887	31.8	492	21	AAB01808	Wheat Mlo homologu
38	886	31.8	450	21	AAB01798	Wheat Mlo homologu
39	801.5	28.7	496	21	AAY44782	Maize MLO3 protein
40	801.5	28.7	496	22	AAU00505	Maize disease resi
41	783.5	28.1	499	21	AAY44606	Maize MLO7 protein
42	765	27.4	224	21	AAY44601	Maize MLO1 protein
43	752.5	27.0	264	20	AAY14140	Zea mays SCLBr pro
44	730.5	26.2	509	20	AAY14138	Zea mays SCLBr pro
45	729.5	26.2	509	21	AAY44603	Maize MLO4 protein

ALIGNMENTS

RESULT 1
AAW59442
ID AAW59442 standard; Protein; 533 AA.
XX
AC AAW59442;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO protein.
XX
KW MLO; mildew; pathogen; resistance.
XX
OS Hordeum vulgare.
XX
PN WO9804586-A2.
XX
PD 05-FEB-1998.
XX
PF 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;
XX
DR WPI; 1998-159149/14.
DR N-PSDB; AAV35022.
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance

XX
PS Claim 1; Fig 2; 150pp; English.
XX
CC The sequence is that encoded by the MLO gene, wild-type Mlo
CC exerts a negative regulatory function on a pathogen defence response,
CC such that mutants exhibit a defence response in the absence of pathogen.
CC Down-regulation or out-competition of Mlo function may be used to
CC stimulate a defence response in transgenic plants conferring increased
CC pathogen resistance, especially resistance to powdery mildew or rust.
CC The product can also be used for identifying compounds able to
CC stimulate a defence response in a plant by interaction with
CC encoded polypeptide.
XX
SQ Sequence 533 AA;

Query Match 100.0%; Score 2788; DB 19; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.1e-293;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
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Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 kaelmlvgfisllliytqdpiiakicisedaadvmwpckrgtegrkpskyvdycpegkva 120

Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 lmstgslhqlhvfifvlavfhvtysvitialsrlkmrtwkkwetettsleyqfandparf 180

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 rfthqtsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlsqnskfdf 240

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 hkyikrsmeddfkvvvgislplwgvailtlfldingvgtliwisfiplvillcvgtklem 300

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 iimemaleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtva 360

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
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Db     361 tpglkkcyhtqiglsimkvvvglalqflcsymtfplyalvtqmgsnmkrsifdeqtskal 420

Qy     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 tnwrntakekkkvrdtdmlmaqmigdatpsrgsspmpsrgsspvhllhkgmgrsddpqsa 480

Qy     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ptsprtqqeardmypvvvahpvhrlnpndrrrsasssaleadipsadfsfsqg 533
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RESULT 2
AAB03401
ID AAB03401 standard; Protein; 533 AA.
XX
AC AAB03401;
XX
DT 27-OCT-2000 (first entry)
XX
DE Barley Mlo protein sequence.
XX
KW Barley; Mlo homologue; disease resistance.
XX
OS Hordeum vulgare.
XX
PN WO200036110-A2.
XX
PD 22-JUN-2000.
XX
PF 17-DEC-1999; 99WO-US30181.
XX
PR 18-DEC-1998; 98US-0112737.
XX
PA (DUPO) DU PONT DE NEMOURS & CO E I.
XX
PI Cahoon RE, Miao G, Rafalski JA, Fang Y, Sakai H, Taramino G;
XX
DR WPI; 2000-431590/37.
XX
PT New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT creating transgenic plants with altered levels of disease resistance -
XX
PS Example 2; Page 72-73; 79pp; English.
XX
CC The present sequence is the barley Mlo sequence. Mlo confers resistance
CC to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation
CC leads to the priming of disease resistance even if the pathogen is not
CC present. The protein, and its gene, can be used to create transgenic
CC plants which have increased disease resistance, as well as allowing
CC researchers to find other resistance-conferring genes and proteins. This
CC sequence was used for this purpose, and potential homologues were
CC obtained in wheat, soybean and rice.
XX
SQ Sequence 533 AA;

Query Match 100.0%; Score 2788; DB 21; Length 533;
Best Local Similarity 100.0%; Pred. No. 1.1e-293;
Matches 533; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 msdkkgvparelpetpswavavvfaamvlvsvlmehglhklghwfqhrhkkalwealekm 60

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 kaelmlvgfisllliytqdpiiakicisedaadvmwpckrgtegrkpskyvdycpegkva 120

Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
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Db     121 lmstgslhqlhvfifvlavfhvtysvitialsrlkmrtwkkwetettsleyqfandparf 180

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 rfthqtsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlsqnskfdf 240

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 hkyikrsmeddfkvvvgislplwgvailtlfldingvgtliwisfiplvillcvgtklem 300

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
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Db     301 iimemaleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtva 360

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
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Db     361 tpglkkcyhtqiglsimkvvvglalqflcsymtfplyalvtqmgsnmkrsifdeqtskal 420

Qy     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
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Qy     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
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Db     481 ptsprtqqeardmypvvvahpvhrlnpndrrrsasssaleadipsadfsfsqg 533
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RESULT 3
AAW59443
ID AAW59443 standard; Protein; 533 AA.

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XX
AC   AAW59443;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO protein.
XX
KW   MLO; mildew; pathogen; resistance.
XX
OS   Hordeum vulgare.
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB02046.
XX
PR   07-MAR-1997;   97GB-0004789.
PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   N-PSDB; AAV35026.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Disclosure; Fig 7; 150pp; English.
XX
CC   The sequence is that encoded by the MLO gene, wild-type Mlo
CC   exerts a negative regulatory function on a pathogen defence response,
CC   such that mutants exhibit a defence response in the absence of pathogen.
CC   Down-regulation or out-competition of Mlo function may be used to
CC   stimulate a defence response in transgenic plants conferring increased
CC   pathogen resistance, especially resistance to powdery mildew or rust.
CC   The product can also be used for identifying compounds able to
CC   stimulate a defence response in a plant by interaction with
CC   encoded polypeptide.
XX
SQ   Sequence   533 AA;
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  Query Match             99.8%;  Score 2782;  DB 19;  Length 533;
  Best Local Similarity   99.8%;  Pred. No. 4.8e-293;
  Matches  532;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Db       1 msdkkgvparelpetpswavavvfaamvlvsvlmehglhklghwfqhrhkkalwealekm 60

Qy      61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDYCPEGKVA 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
           |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 lmstgslhqlhvlifvlavfhvtysvitialsrlkmrtwkkwetettsleyqfandparf 180

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 rfthqtsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlsqnskfdf 240

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 hkyikrsmeddfkvvvgislplwgvailtlfldingvgtliwisfiplvillcvgtklem 300

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     301 iimemaleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtva 360

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     361 tpglkkcyhtqiglsimkvvvglalqflcsymtfplyalvtqmgsnmkrsifdeqtskal 420

Qy     421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 tnwrntakekkkvrdtdmlmaqmigdatpsrgsspmpsrgsspvhllhkgmgrsddpqsa 480

Qy     481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     481 ptsprtqqeardmypvvvahpvhrlnpndrrrsasssaleadipsadfsfsqg 533
```

```
RESULT   4
AAB01805
ID   AAB01805 standard; Protein; 534 AA.
XX
AC   AAB01805;
XX
DT   27-OCT-2000  (first entry)
XX
DE   Wheat Mlo homologue putative protein sequence #4.
XX
KW   Wheat; Mlo homologue; disease resistance.
XX
OS   Triticum aestivum.
XX
PN   WO200036110-A2.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US30181.
XX
PR   18-DEC-1998;   98US-0112737.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE,  Miao G,  Rafalski JA,  Fang Y,  Sakai H,  Taramino G;
XX
DR   WPI; 2000-431590/37.
DR   N-PSDB; AAA52715.
XX
PT   New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT   creating transgenic plants with altered levels of disease resistance -
XX
PS   Claim 10; Page 64-66; 79pp; English.
XX
CC   The present sequence is a putative protein sequence for a Mlo homologue
CC   from wheat. Its coding sequence was identified by searching a root and
CC   leaf cDNA library for sequences encoding proteins similar to Mlo from
CC   Hordeum vulgare (barley) and Arabidopsis thaliana. Mlo confers resistance
CC   to Erysiphe graminis f. sp. hordei upon the plant, and its inactivation
CC   leads to the priming of disease resistance even if the pathogen is not
CC   present. The gene and protein can be used to create transgenic plants
CC   which have increased disease resistance, as well as allowing researchers
CC   to find other resistance-conferring genes and proteins.
XX
SQ   Sequence   534 AA;
```

```
  Query Match             87.3%;  Score 2434;  DB 21;  Length 534;
  Best Local Similarity   89.2%;  Pred. No. 3.2e-255;
  Matches  471;  Conservative   20;  Mismatches   33;  Indels    4;  Gaps    3;

Qy       8 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLV 67
           ||| |||||||||:||| |::||||:|| |||||||| ||| || |||||:|||||||
Db       9 partlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekikaelmlv 68

Qy      68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
           ||||||| ||||| |: ||||| || :| ||     |   ||| ||    :|||:|||||
Db      69 gfisillavtqdp-isgicisekaasimrpcsl-ppgsvkskykdyycakkgkvslmstg 126
```

```
Qy    126 SLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
          ||||||:|||||||||||||||| :|||||||||||||||| ||||||||||||||||||
Db    127 slhqlhififvlavfhvtysviimalsrlkmrtwkkwetetasleyqfandparfrfthq 186

Qy    186 TSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245
          ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db    187 tsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlshnskfdfhkyik 246

Qy    246 RSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEM 305
          |||||||||||||||||| |||||||||:|:||| ||||||||||||||||||||||||
Db    247 rsmeddfkvvvgislplwcvailtlfldidgigtltwisfiplvillcvgtklemiimem 306

Qy    306 ALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 365
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 aleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtvatpglk 366

Qy    366 KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN 425
          ||:|  |||||||||:|||||||||:|||||||||||||||||||||:||||||||
Db    367 kcfhmhiglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakaltnwrn 426

Qy    426 TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485
          |||||||||||||||||||||||||:|||||| ||||||||||||||||||||||||||
Db    427 takekkkvrdtdmlmaqmigdatpsrgtspmpsrasspvhllhkgmgrsddpqsaptspr 486

Qy    486 TQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
          | :|||||||||||||||| ||||| |||||:||||||||||||
Db    487 tmeeardmypvvvahpvhrlnpadrrrsvsssaldadipsadfsfsqg 534
```

RESULT 5
AAY26966
ID AAY26966 standard; Protein; 534 AA.
XX
AC AAY26966;
XX
DT 21-DEC-1999 (first entry)
XX
DE Wheat Mlo fungal resistance protein TrMlo1.
XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW Mlo; Erysiphe graminis; powdery mildew.
XX
OS Triticum sp.
XX
PN WO9947552-A2.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99WO-EP01779.
XX
PR 17-MAR-1998; 98US-0042763.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX
DR WPI; 1999-571820/48.
DR N-PSDB; AAZ30409.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 58-60; 102pp; English.
XX
CC This sequence represents the wheat fungal resistance protein TrMlo1,
CC which confers resistance to fungal pathogens by stimulating the formation
CC of large cell wall appositions, designated papillae, at the contact site
CC with the fungal pathogen. These papillae mainly contain callose, but
CC also contain carbohydrate, phenols and proteins and are used to prevent
CC penetration of the fungal hyphae into the plant. The new Mlo sequences
CC are used to generate transgenic plants resistant to fungal pathogens,
CC especially Erysiphe graminis (powdery mildew).
XX
SQ Sequence 534 AA;

Query Match 87.3%; Score 2433; DB 20; Length 534;
Best Local Similarity 88.2%; Pred. No. 4.1e-255;
Matches 470; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

```
Qy      3 DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62
          | :  ||| |||||||||:||| |::||||:|| |||||||  ||| || |||||:||
Db      4 ddeyppartlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekika 63

Qy     63 ELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVA 120
          |||||||||||| ||||| |: ||||| || :| |||    |   ||| ||    :|||:
Db     64 elmlvgfislllavtqdp-isgicisekaasimrpckl-ppgsvkskykdyycakqgkvs 121

Qy    121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
          ||||||||||:|||||||||||||| :|||||||||||||| ||||||||||||
Db    122 lmstgslhqlhifififvlavfhvtysviimalsrlkmrtwkkwetetasleyqfandparf 181

Qy    181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
          |||||||||||||||||||:|||||||||||||||||||||||||||||| ||||||
Db    182 rfthqtsfvkrhlglsstpgvrwvvaffrqffrsvtkvdyltlragfinahlshnskfdf 241

Qy    241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
          |||||||||||||||||||| ||||||||||:|:||| ||||||||||||||||||||
Db    242 hkyikrsmeddfkvvvgislplwcvailtlfldidgigtltwisfiplvillcvgtklem 301

Qy    301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 iimemaleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtva 361

Qy    361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
          |||||||:|  |||||||||:||||||||||:|||||||||||||||||||||||:|||
Db    362 tpglkkcfhmhiglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakal 421

Qy    421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
          ||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db    422 tnwrntakekkkvrdtdmlmaqmigdatpsrgaspmpsrgsspvhllhkgmgrsddpqst 481

Qy    481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
          |||||  :|||||||||||||||| ||||| |||||: ||||||||||||
Db    482 ptsprameeardmypvvvahpvhrlnpadrrrsvsssaldvdipsadfsfsqg 534
```

RESULT 6
AAY26968
ID AAY26968 standard; Protein; 534 AA.
XX
AC AAY26968;
XX
DT 21-DEC-1999 (first entry)
XX
DE Wheat Mlo fungal resistance protein TrMlo3.
XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW Mlo; Erysiphe graminis; powdery mildew.
XX
OS Triticum sp.
XX
PN WO9947552-A2.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99WO-EP01779.
XX
PR 17-MAR-1998; 98US-0042763.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX
DR WPI; 1999-571820/48.
DR N-PSDB; AAZ30411.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 68-70; 102pp; English.
XX
CC This sequence represents the wheat fungal resistance protein TrMlo3,
CC which confers resistance to fungal pathogens by stimulating the formation
CC of large cell wall appositions, designated papillae, at the contact site
CC with the fungal pathogen. These papillae mainly contain callose, but
CC also contain carbohydrate, phenols and proteins and are used to prevent
CC penetration of the fungal hyphae into the plant. The new Mlo sequences
CC are used to generate transgenic plants resistant to fungal pathogens,
CC especially Erysiphe graminis (powdery mildew).
XX
SQ Sequence 534 AA;

Query Match 87.3%; Score 2433; DB 20; Length 534;
Best Local Similarity 88.8%; Pred. No. 4.1e-255;
Matches 469; Conservative 22; Mismatches 33; Indels 4; Gaps 3;

```
Qy       8 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLV 67
Db       9 partlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekmkaelmlv 68

Qy      68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
Db      69 gfislllavtqdp-isgicisqkaasimrpck-vepgsvkskykdyycakegkvalmstg 126

Qy     126 SLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
Db     127 slhqlhififvlavfhvtysviimalsrlkmrtwkkwetetasleyqfandparfrfthq 186

Qy     186 TSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245
Db     187 tsfvkrhlglsstpgvrwvvaffrqffrsvtkvdyltlragfinahlsqnskfdfhkyik 246

Qy     246 RSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEM 305
Db     247 rsmeddfkvvvgislplwavailtlfldidgigtltwvsfipliillcvgtklemiimgm 306

Qy     306 ALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 365
Db     307 aleiqdrssvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtvatpglk 366

Qy     366 KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN 425
Db     367 dcfhmniglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakaltnwrn 426

Qy     426 TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485
Db     427 takekkkvrdtdmlmaqmigdatpsrgtspmpsrgsspvhllqkgmgrsddpqsaptspr 486

Qy     486 TQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
Db     487 tmeeardmypvvvahpvhrlnpadrrrsvsssaldadipsadfsfsqg 534
```

RESULT 7
AAB31250
ID AAB31250 standard; Protein; 534 AA.
XX
AC AAB31250;
XX
DT 20-APR-2001 (first entry)
XX
DE Amino acid sequence of the wheat Mlo protein TrMlo1.

XX
KW Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW powdery mildew; Mlo; cell wall apposition; transgenic plant.
XX
OS Triticum sp.
XX
PN WO200078799-A2.
XX
PD 28-DEC-2000.
XX
PF 16-JUN-2000; 2000WO-EP05576.
XX
PR 18-JUN-1999; 99US-0336112.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM, Wang HX;
PI Vernooij BT, Levin JZ, Heifetz PB, Patton DA, Que Q;
XX
DR WPI; 2001-112311/12.
DR N-PSDB; AAF24583.
XX
PT Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT producing fungal resistant plants, in particular wheat plant -
XX
PS Claim 12; Page 90-92; 128pp; English.
XX
CC The present sequence represents a Mlo protein. Mlo proteins given
CC resistance to fungal pathogens which infect living epidermal plant cells.
CC Mlo proteins give proteins resistance to fungal pathogens, especially
CC Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC locus are responsible for a plant resistant pathotype. The mechanism
CC of Mlo resistance involves the formation of large cell wall appositions,
CC called papillae, at pathogen contact sites. Papillae mainly contain
CC callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC encoding Mlo proteins are useful for making transgenic plants,
CC preferably wheat, which are resistant to fungal pathogens.
XX
SQ Sequence 534 AA;

Query Match 87.3%; Score 2433; DB 22; Length 534;
Best Local Similarity 88.2%; Pred. No. 4.1e-255;
Matches 470; Conservative 22; Mismatches 37; Indels 4; Gaps 3;

```
Qy       3 DKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKA 62
Db       4 ddeyppartlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekika 63

Qy      63 ELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVA 120
Db      64 elmlvgfislllavtqdp-isgicisekaasimrpckl-ppgsvkskykdyycakqgkvs 121

Qy     121 LMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARF 180
Db     122 lmstgslhqlhififvlavfhvtysviimalsrlkmrtwkkwetetasleyqfandparf 181

Qy     181 RFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDF 240
Db     182 rfthqtsfvkrhlglsstpgvrwvvaffrqffrsvtkvdyltlragfinahlshnskfdf 241

Qy     241 HKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEM 300
Db     242 hkyikrsmeddfkvvvgislplwcvailtlfldidgigtltwisfiplvillcvgtklem 301

Qy     301 IIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVA 360
Db     302 iimemaleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtva 361

Qy     361 TPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKAL 420
Db     362 tpglkkcfhmhiglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakal 421
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Qy    421 TNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSA 480
          ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||
Db    422 tnwrntakekkkvrdtdmlmaqmigdatpsrgaspmpsrgsspvhllhkgmgrsddpqst 481

Qy    481 PTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
          |||||  :|||||||||||||||||||| ||||| |||||: ||||||||||||
Db    482 ptsprameeardmypvvvahpvhrlnpadrrrsvsssaldvdipsadfsfsqg 534


RESULT   8
AAB31252
ID   AAB31252 standard; Protein; 534 AA.
XX
AC   AAB31252;
XX
DT   20-APR-2001  (first entry)
XX
DE   Amino acid sequence of the wheat Mlo protein TrMlo3.
XX
KW   Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW   powdery mildew; Mlo; cell wall apposition; transgenic plant.
XX
OS   Triticum sp.
XX
PN   WO200078799-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-EP05576.
XX
PR   18-JUN-1999;   99US-0336112.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM,  Wang HX;
PI   Vernooij BT,  Levin JZ,  Heifetz PB,  Patton DA,  Que Q;
XX
DR   WPI; 2001-112311/12.
DR   N-PSDB; AAF24585.
XX
PT   Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT   producing fungal resistant plants, in particular wheat plant  -
XX
PS   Claim 12; Page 99-101; 128pp; English.
XX
CC   The present sequence represents a Mlo protein. Mlo proteins given
CC   resistance to fungal pathogens which infect living epidermal plant cells.
CC   Mlo proteins give proteins resistance to fungal pathogens, especially
CC   Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC   locus are responsible for a plant resistant pathotype. The mechanism
CC   of Mlo resistance involves the formation of large cell wall appositions,
CC   called papillae, at pathogen contact sites. Papillae mainly contain
CC   callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC   encoding Mlo proteins are useful for making transgenic plants,
CC   preferably wheat, which are resistant to fungal pathogens.
XX
SQ   Sequence   534 AA;


  Query Match             87.3%;  Score 2433;  DB 22;  Length 534;
  Best Local Similarity   88.8%;  Pred. No. 4.1e-255;
  Matches  469;  Conservative   22;  Mismatches   33;  Indels    4;  Gaps    3;

Qy      8 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLV 67
          ||| |||||||||||:||| |::||||:|| |||||||| ||| || ||||||||||||||
Db      9 partlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekmkaelmlv 68

Qy     68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
          ||||||| ||||| |: |||| || :| |||    |   ||| ||    ||||||||||
Db     69 gfislllavtqdp-isgicisqkaasimrpck-vepgsvkskykdyycakegkvalmstg 126

Qy    126 SLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
          |||||:|||||||||||||| :|||||||||||||||| ||||||||||||||||||||
Db    127 slhqlhififvlavfhvtysviimalsrlkmrtwkkwetetasleyqfandparfrfthq 186

Qy    186 TSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245
          ||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||
Db    187 tsfvkrhlglsstpgvrwvvaffrqffrsvtkvdyltlragfinahlsqnskfdfhkyik 246

Qy    246 RSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEM 305
          |||||||||||||||| |||||||||:|:||| |:|||||:||||||||||||||| |
Db    247 rsmeddfkvvvgislplwavailtlfldidgigtltwvsfipliillcvgtklemiimgm 306

Qy    306 ALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 365
          |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    307 aleiqdrssvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtvatpglk 366

Qy    366 KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN 425
          |:|  |||||||||:|||||||||:|||||||||||||||||||||||||:||||||||
Db    367 dcfhmniglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakaltnwrn 426

Qy    426 TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485
          ||||||||||||||||||||||||||:||||||||||| ||||||||||||||||||||
Db    427 takekkkvrdtdmlmaqmigdatpsrgtspmpsrgsspvhllqkgmgrsddpqsaptspr 486

Qy    486 TQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
          | :|||||||||||||||||| ||||| ||||||:||||||||||||||
Db    487 tmeeardmypvvvahpvhrlnpadrrrsvsssaldadipsadfsfsqg 534


RESULT   9
AAY26967
ID   AAY26967 standard; Protein; 534 AA.
XX
AC   AAY26967;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Wheat Mlo fungal resistance protein TrMlo2.
XX
KW   Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW   papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW   Mlo; Erysiphe graminis; powdery mildew.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 168
FT                   /label= unknown
FT                   /note= "encoded by GYC"
XX
PN   WO9947552-A2.
XX
PD   23-SEP-1999.
XX
PF   17-MAR-1999;   99WO-EP01779.
XX
PR   17-MAR-1998;   98US-0042763.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM;
XX
DR   WPI; 1999-571820/48.
DR   N-PSDB; AAZ30410.
XX
PT   New proteins useful for generating transgenic plants resistant to
PT   fungal infection  -
XX
PS   Claim 2; Page 63-65; 102pp; English.
XX
CC   This sequence represents the wheat fungal resistance protein TrMlo2,
CC   which confers resistance to fungal pathogens by stimulating the formation
```

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CC   of large cell wall appositions, designated papillae, at the contact site
CC   with the fungal pathogen. These papillae mainly contain callose, but
CC   also contain carbohydrate, phenols and proteins and are used to prevent
CC   penetration of the fungal hyphae into the plant. The new Mlo sequences
CC   are used to generate transgenic plants resistant to fungal pathogens,
CC   especially Erysiphe graminis (powdery mildew).
XX
SQ   Sequence   534 AA;


  Query Match             87.2%;  Score 2432;  DB 20;  Length 534;
  Best Local Similarity   89.2%;  Pred. No. 5.3e-255;
  Matches  471;  Conservative   20;  Mismatches   33;  Indels    4;  Gaps    3;

Qy       8 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLV 67
           ||| |||||||||||:||| |::||||:|| |||||||| ||| || |||||:|||||||
Db       9 partlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekikaelmlv 68

Qy      68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
           ||||||| ||||| |: ||||| || :| ||      |   ||| ||    :|||:|||||
Db      69 gfislllavtqdp-isgicisekaasimrpcsl-ppgsvkskykdyycakkgkvslmstg 126

Qy     126 SLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
           ||||||:|||||||||||||| :|||||||||||||| |||||||||||||||||||||
Db     127 slhqlhmfifvlavfhvtysviimalsrlkmrtwkkwetetxsleyqfandparfrfthq 186

Qy     186 TSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     187 tsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlshnskfdfhkyik 246

Qy     246 RSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEM 305
           |||||||||||||||| |||||||||:|:||| ||||||||||||||||||||||||||
Db     247 rsmeddfkvvvgislplwcvailtlfldidgigtltwisfiplvillcvgtklemiimem 306

Qy     306 ALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 aleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtvatpglk 366

Qy     366 KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN 425
           ||:|  |||||||||:||||||||||:|||||||||||||||||||||||:||||||||
Db     367 kcfhmhiglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakaltnwrn 426

Qy     426 TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485
           ||||||||||||||||||||||||||:|||||| ||||||||||||||||||||||||||
Db     427 takekkkvrdtdmlmaqmigdatpsrgtspmpsrasspvhllhkgmgrsddpqsaptspr 486

Qy     486 TQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
           | :|||||||||||||||||| ||||| ||||:|||||||||||||
Db     487 tmeeardmypvvvahpvhrlnpadrrrsvsssaldadipsadfsfsqg 534


RESULT  10
AAB31251
ID   AAB31251 standard; Protein; 534 AA.
XX
AC   AAB31251;
XX
DT   20-APR-2001  (first entry)
XX
DE   Amino acid sequence of the wheat Mlo protein TrMlo2.
XX
KW   Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW   powdery mildew; Mlo; cell wall apposition; transgenic plant.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 168
FT                   /note= "unspecified amino acid encoded by GYC"
XX
PN   WO200078799-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-EP05576.
XX
PR   18-JUN-1999;   99US-0336112.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM,  Wang HX;
PI   Vernooij BT,  Levin JZ,  Heifetz PB,  Patton DA,  Que Q;
XX
DR   WPI; 2001-112311/12.
DR   N-PSDB; AAF24584.
XX
PT   Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT   producing fungal resistant plants, in particular wheat plant  -
XX
PS   Claim 12; Page 94-96; 128pp; English.
XX
CC   The present sequence represents a Mlo protein. Mlo proteins given
CC   resistance to fungal pathogens which infect living epidermal plant cells.
CC   Mlo proteins give proteins resistance to fungal pathogens, especially
CC   Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC   locus are responsible for a plant resistant pathotype. The mechanism
CC   of Mlo resistance involves the formation of large cell wall appositions,
CC   called papillae, at pathogen contact sites. Papillae mainly contain
CC   callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC   encoding Mlo proteins are useful for making transgenic plants,
CC   preferably wheat, which are resistant to fungal pathogens.
XX
SQ   Sequence   534 AA;


  Query Match             87.2%;  Score 2432;  DB 22;  Length 534;
  Best Local Similarity   89.2%;  Pred. No. 5.3e-255;
  Matches  471;  Conservative   20;  Mismatches   33;  Indels    4;  Gaps    3;

Qy       8 PARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLV 67
           ||| |||||||||||:||| |::||||:|| |||||||| ||| || |||||:|||||||
Db       9 partlpetpswavalvfavmiivsvllehalhklghwfhkrhknalaealekikaelmlv 68

Qy      68 GFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSKYVDY--CPEGKVALMSTG 125
           ||||||| ||||| |: ||||| || :| ||      |   ||| ||    :|||:|||||
Db      69 gfislllavtqdp-isgicisekaasimrpcsl-ppgsvkskykdyycakkgkvslmstg 126

Qy     126 SLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQ 185
           ||||||:|||||||||||||| :|||||||||||||| |||||||||||||||||||||
Db     127 slhqlhmfifvlavfhvtysviimalsrlkmrtwkkwetetxsleyqfandparfrfthq 186

Qy     186 TSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIK 245
           |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db     187 tsfvkrhlglsstpgirwvvaffrqffrsvtkvdyltlragfinahlshnskfdfhkyik 246

Qy     246 RSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEM 305
           |||||||||||||||| |||||||||:|:||| ||||||||||||||||||||||||||
Db     247 rsmeddfkvvvgislplwcvailtlfldidgigtltwisfiplvillcvgtklemiimem 306

Qy     306 ALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLK 365
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     307 aleiqdrasvikgapvvepsnkffwfhrpdwvlffihltlfqnafqmahfvwtvatpglk 366

Qy     366 KCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRN 425
           ||:|  |||||||||:||||||||||:|||||||||||||||||||||||:||||||||
Db     367 kcfhmhiglsimkvvlglalqflcsyitfplyalvtqmgsnmkrsifdeqtakaltnwrn 426

Qy     426 TAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPR 485
           ||||||||||||||||||||||||||:|||||| ||||||||||||||||||||||||||
Db     427 takekkkvrdtdmlmaqmigdatpsrgtspmpsrasspvhllhkgmgrsddpqsaptspr 486

Qy     486 TQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADIPSADFSFSQG 533
           | :|||||||||||||||||| ||||| ||||:|||||||||||||
Db     487 tmeeardmypvvvahpvhrlnpadrrrsvsssaldadipsadfsfsqg 534
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```
RESULT  11
AAW59445
ID   AAW59445 standard; Protein; 544 AA.
XX
AC   AAW59445;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO protein homologue.
XX
KW   MLO; mildew; pathogen; resistance.
XX
OS   Hordeum vulgare.
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB02046.
XX
PR   07-MAR-1997;   97GB-0004789.
PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   N-PSDB; AAV35030.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Claim 8; Fig 14; 150pp; English.
XX
CC   The sequence is that encoded by a homologue of the MLO gene, wild-type
CC   Mlo exerts a negative regulatory function on a pathogen defence response,
CC   such that mutants exhibit a defence response in the absence of pathogen.
CC   Down-regulation or out-competition of Mlo function may be used to
CC   stimulate a defence response in transgenic plants conferring increased
CC   pathogen resistance, especially resistance to powdery mildew or rust.
CC   The product can also be used for identifying compounds able to
CC   stimulate a defence response in a plant by interaction with
CC   encoded polypeptide.
XX
SQ   Sequence   544 AA;

  Query Match             69.1%;  Score 1927;  DB 19;  Length 544;
  Best Local Similarity   69.2%;  Pred. No. 4.3e-200;
  Matches  379;  Conservative   51;  Mismatches   78;  Indels   40;  Gaps    6;

Qy      10 RELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELMLVGF 69
           ||| :||:|||||| | |:|||| ||| |||||||    |||| ||||||||||||||
Db       8 relsdtptwavavvcavmilvsvamehalhklghwfhkwrkkalgealekmkaelmlvgf 67

Qy      70 ISLLLIVTQDPIIAKICISEDAADVMWPCK--------RGTEGRKPSKY---------- 110
           |||||||||||| :::|||::| : | |||        :| :  :   :
Db      68 islllivtqdp-vsriciskeagekmlpckpydgagggkgkdnhrrllwlqgesethrrf 126

Qy     111 ------VDYC-PEGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWE 163
                 || |  :|||||| ||:|||||:|||||||||| |||:|: |||||: | |||
Db     127 laapagvdvcakqgkvalmsagsmhqlhififvlavfhvlysvvtmtlsrlkmkqwnkwe 186

Qy     164 TETTSLEYQFANDPARFRFTHQTSFVKRHLGLSSTPGIRWVVAFFRQFFRSVTKVDYLTL 223
           :|| ||||||||||:| |||||: |:||||||||||:|||||||||| ||||||||||
Db     187 setasleyqfandpsrcrfthqttlvrrhlglsstpgvrwvvaffrqfftsvtkvdyltl 246

Qy     224 RAGFINAHLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWI 283
           | |||||||||| ::||| ||||||:|||||||| ||| || ||:| |||| :|:|||:|:

Db     247 rqgfinahlsqgnrfdfdkyikrsleddfkvvvrislklwfvavlilfldfdgigtllwm 306

Qy     284 SFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHL 343
           | :|||||| |||||||:|||| || || ||:|||| ||||||:|||:|||||||| :||
Db     307 svvplvillwvgtklemvimemaqeihdresvvkgapavepsnkyfwfnrpdwvlflmhl 366

Qy     344 TLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQM 403
           |||||||||||||||||||||||||| :: :|| |||:|:|  | ||||:||||||||||
Db     367 tlfqnafqmahfvwtvatpglkkcyhekmamsiakvvlgvaaqilcsyitfplyalvtqm 426

Qy     404 GSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSP 463
           ||:|||||||||:|||||||  |||||| ||  |||||  | ||        || ||||
Db     427 gshmkrsifdeqtakaltnwrkmakekkkardaamlmaqmgggat--------psvgssp 478

Qy     464 VHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHPVHRLNPNDRRRSASSSALEADI 523
           ||||||   ||||||| | ||| ::|        | ||  :: | |  ||||| ||:| |
Db     479 vhllhkagarsddpqsvpaspraekeggg-----vqhparkvppcdgwrsasspaldahi 533

Qy     524 PSADFSFS 531
           | ||| ||
Db     534 pgadfgfs 541


RESULT  12
AAW59444
ID   AAW59444 standard; Protein; 536 AA.
XX
AC   AAW59444;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Oryza sativa MLO protein homologue.
XX
KW   MLO; mildew; pathogen; resistance.
XX
OS   Oryza sativa.
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB02046.
XX
PR   07-MAR-1997;   97GB-0004789.
PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   N-PSDB; AAV35028.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Claim 5; Fig 13; 150pp; English.
XX
CC   The sequence is that encoded by a homologue of the MLO gene, wild-type
CC   Mlo exerts a negative regulatory function on a pathogen defence response,
CC   such that mutants exhibit a defence response in the absence of pathogen.
CC   Down-regulation or out-competition of Mlo function may be used to
CC   stimulate a defence response in transgenic plants conferring increased
CC   pathogen resistance, especially resistance to powdery mildew or rust.
CC   The product can also be used for identifying compounds able to
CC   stimulate a defence response in a plant by interaction with
CC   encoded polypeptide.
XX
SQ   Sequence   536 AA;
```

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  Query Match             63.4%;  Score 1767.5;  DB 19;  Length 536;
  Best Local Similarity   66.8%;  Pred. No. 9.1e-183;
  Matches  364;  Conservative   55;  Mismatches   85;  Indels   41;  Gaps   13;

Qy       9 ARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEAL----EKMKAEL 64
           :|||||||:|||||| | :||||  |||||| | |        |   | |         |||
Db       8 srelpetptwavavvcavlvlvsaamehglhnlsh-------kttaevliflvlsalael 60

Qy      65 MLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTE--------GRKPSKYV---DY 113
           ||:|||||||  | | | |:|||| : ||::: ||| | :        ||:         ||
Db      61 mllgfisllltvaqap-iskicipksaanillpckagqdaieeeaasgrrslagagggdy 119

Qy     114 CP--EGKVALMSTGSLHQLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEY 171
           |   :|||||||  |:||||:||||||||||||| :||: | ||||: |||||::| ||||
Db     120 cskfdgkvalmsaksmhqlhififvlavfhvtyciitmglgrlkmkkwkkwesqtnsley 179

Qy     172 QFANDPARFRFTHQTSFVKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINA 230
           ||| ||:|||||||||||||||  |||||:||:|||||||| |||||||||:| |||||
Db     180 qfaidpsrfrfthqtsfvkrhlgsfsstpglrwivaffrqffgsvtkvdyltmrqgfina 239

Qy     231 HLSQNSKFDFHKYIKRSMEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVI 290
           ||||||||||||||||:|||||||||||||| | || |||||:|:||||||||:||:|
Db     240 hlsqnskfdfhkyikrsleddfkvvvgislplwfvgilvlfldihglgtliwisfvplii 299

Qy     291 LLCVGTKLEMIIMEMALEIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAF 350
           :| |||||||:||||| ||||||:||:|||:|||||||:|||:|||||||||||||| |||
Db     300 vllvgtklemvimemaqeiqdratviqgapmvepsnkyfwfnrpdwvlffihltlfhnaf 359

Qy     351 QMAHFVWTVATPGLKKCYHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRS 410
           ||||||||:|||||||:|  | |||::|:||::|| ||||:|||||||||||||||:: 
Db     360 qmahfvwtmatpglkkcfheniwlsivevivgislqvlcsyitfplyalvtqmgsnmkkt 419

Qy     411 IFDEQTSKALTNWRNTAKEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSSPVHLLHKG 470
           ||:||| ||| |||  | |||||| |  :|||  |      ::|  || :|||||| :
Db     420 ifeeqtmkalmnwrkkamekkkvrdadaflaqmsvdf-----atpassrsaspvhll-qv 473

Qy     471 MGRSDDPQSAPT--SPRTQQEARDMYPVVVAHPVHRL--NPNDRRRSASSSALEADIPSA 526
             ||   | |  |  ||   :|  ||||| |    :|  :| ||| ||||   ||| :
Db     474 tgrvgrppspitvasppapee--dmypvpaaaasrqllddppdrrwmasss---adiads 528

Qy     527 DFSFS 531
           |||||
Db     529 dfsfs 533


RESULT  13
AAY14139
ID   AAY14139 standard; Protein; 515 AA.
XX
AC   AAY14139;
XX
DT   22-JUL-1999  (first entry)
XX
DE   Zea mays SCLBr protein clone ctal.pk0005.c1.
XX
KW   SCLBr protein; southern corn leaf blight resistance; leaf blight disease;
KW   fungus; Helminthosporium maydis; corn; resistance.
XX
OS   Zea mays.
XX
PN   WO9923235-A1.
XX
PD   14-MAY-1999.
XX
PF   02-NOV-1998;   98WO-US23195.
XX
PR   05-NOV-1997;   97US-0064492.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE,  Miao G,  Rafalski JA,  Taramino G;
XX
DR   WPI; 1999-313350/26.
DR   N-PSDB; AAX58274.
XX
PT   Zea mays cDNA encoding southern corn leaf blight resistance protein
XX
PS   Claim 5; Page 44-45; 52pp; English.
XX
CC   This sequence is a southern corn leaf blight resistance (SCLBr)
CC   protein of the invention. A chimeric gene containing the SCLBr coding
CC   sequence, can be used to alter the level of expression of a SCLBr protein
CC   in a host cell. The nucleic acid fragments can be used as probes, or to
CC   synthesize primers, to obtain further nucleic acid fragments or
CC   homologues encoding all or a substantial portion of the amino acid
CC   sequence encoding a SCLBr protein. The polynucleotides are useful for the
CC   production of transgenic plants having altered resistance to certain
CC   diseases, such as leaf blight disease caused by the fungus
CC   Helminthosporium maydis in corn (Zea mays).
XX
SQ   Sequence   515 AA;


  Query Match             45.1%;  Score 1257;  DB 20;  Length 515;
  Best Local Similarity   48.7%;  Pred. No. 2.6e-127;
  Matches  251;  Conservative   84;  Mismatches  116;  Indels   64;  Gaps    7;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |  :||| :||:|||| |   :||:|:|:| ||| :| :| || ||||: |||||:|||||
Db       7 ggnsreldqtptwavasvcgvivlisillekglhhvgeffshrkkkamvealekvkaelm 66

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK----------RGTE---------- 103
           ::|||||||:  |: || |:|||  ||: | |||           | |
Db      67 vlgfislllvfgqnyii-kvcisnhaantmlpckleaaavegkdghgkeaaavvagkkkv 125

Qy     104 -----GRKPSK----------YVDY--------------------CPEGKVALMSTGSLH 128
                 |:|  |           ||:                    |||||| |:|  :||
Db     126 avavpgkkkkkaaaaadhlggvvdwpppyyahnarmlaeasmatkcpegkvplisinalh 185

Qy     129 QLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSF 188
           |||:||| ||||||:|| ||:|| | |:| ||:|| |    :|:|::|| |||||||:|||
Db     186 qlhifiifflavfhvsysaitmalgrakirawkewekeaagqdyefshdptrfrfthetsf 245

Qy     189 VKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRS 247
           |::|:  |:  |   ::  ||||||||| : ||  ||  |:| ||:  ||||| ||||||
Db     246 vrqhmnvlnkfpasfyisnffrqffrsvrqadycalrhsfvnvhlapgskfdfqkyikrs 305

Qy     248 MEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMAL 307
           :||||||:|||| ||| |:: |||::||  |::||| :|:||:| ||||||: ||  ||:
Db     306 leddfkvivgispplwasaliflflnvngwhtmlwisimpvviilsvgtklqggiicrmai 365

Qy     308 EIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKC 367
           :| :| :||:| |:|: |: :||| || :||| || ||||| ||: :|:| :   |:  |
Db     366 diterhaviqgipmvqvsdsyfwfarptfvlflihftlfqngfqiiyflwilyeygmdsc 425

Qy     368 YHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTA 427
           ::       :: :|: :| ||||:| ||||||:|||| ||:||||||||||| ||| |
Db     426 fndseefvfarlclgvvvqvlcsyvtlplyalvsqmgstmkqsifdeqtskalknwraga 485

Qy     428 KEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS 462
           |:|          ::  |  :|: | ||  : | :
Db     486 kkkaptgg-----skhggggsptaggsptkadgda 515


RESULT  14
AAY44605
ID   AAY44605 standard; Protein; 515 AA.
XX
AC   AAY44605;
XX
DT   07-APR-2000  (first entry)
XX
DE   Maize MLO6 protein.
XX
KW   MLO6 protein; ZmMLO6; chromosome 5; mutation; recessive allele;
KW   disease resistance; pathogen; anti-infective; antipathogenic; antiviral;
```

```
KW   antifungal; antihelminthic; anti-arthropod; maize; HvMLO1.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   Region          1..18
FT                   /label= N-terminal_region
FT   Domain          19..36
FT                   /label= Transmembrane_helix_1
FT   Region          37..65
FT                   /label= Intervening_region_1
FT   Domain          66..89
FT                   /label= Transmembrane_helix_2
FT   Region          90..189
FT                   /label= Intervening_region_2
FT   Domain          190..209
FT                   /label= Transmembrane_helix_3
FT   Region          210..311
FT                   /label= Intervening_region_3
FT   Domain          312..330
FT                   /label= Transmembrane_helix_4
FT   Region          331..337
FT                   /label= Intervening_region_4
FT   Domain          338..354
FT                   /label= Transmembrane_helix_5
FT   Region          355..435
FT                   /label= Intervening_region_5
FT   Domain          436..459
FT                   /label= Transmembrane_helix_6
FT   Region          460..515
FT                   /label= C-terminal_region
XX
PN   WO200001722-A1.
XX
PD   13-JAN-2000.
XX
PF   07-JUL-1999;   99WO-US15255.
XX
PR   07-JUL-1998;   98US-0091875.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Briggs SP,  Simmons CR;
XX
DR   WPI; 2000-137196/12.
DR   N-PSDB; AAZ49564.
XX
PT   Creating or enhancing disease resistance in plants by modulating plant
PT   resistance genes expression  -
XX
PS   Claim 1b; Page 71-73; 88pp; English.
XX
CC   The present sequence is the maize MLO6 (ZmMLO6) protein, which exhibits
CC   sequence homology to barley MLO1 (HvMLO1) sequence. MLO6 protein is
CC   encoded by a mutation-induced recessive allele Mlo6, located on
CC   chromosome 5, that confers resistance to plant pathogens. Expression of
CC   native Mlo genes in plants can be altered by transforming them with a
CC   DNA construct comprising the mutated Mlo gene. Decreasing the expression
CC   or activity of native MLO protein leads to enhanced resistance of plants
CC   against pathogens such as fungi, virus, nematodes and insects. Mlo gene
CC   can be used to isolate related sequences from other plants and as
CC   molecular markers used in breeding programs aimed at improving disease
CC   resistance. MLO protein has anti-infective, antipathogenic, antiviral,
CC   antifungal, antihelminthic and anti-arthropod activity.
XX
SQ   Sequence   515 AA;

  Query Match             45.1%;  Score 1257;  DB 21;  Length 515;
  Best Local Similarity   48.7%;  Pred. No. 2.6e-127;
  Matches  251;  Conservative   84;  Mismatches  116;  Indels   64;  Gaps    7;

Qy       6 GVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKMKAELM 65
           |  :||| :||:|||| |   :||:|:|:| ||| :| :| || |||: |||||:|||||
Db       7 ggnsreldqtptwavasvcgvivlisillekglhhvgeffshrkkkamvealekvkaelm 66

Qy      66 LVGFISLLLIVTQDPIIAKICISEDAADVMWPCK----------RGTE---------- 103
           ::|||||||:  |: || |:||| ||: | |||           | |
Db      67 vlgfisllvfgqnyii-kvcisnhaantmlpckleaaavegkdghgkeaaavvagkkkv 125

Qy     104 -----GRKPSK----------YVDY-------------------CPEGKVALMSTGSLH 128
            |:|  |           ||:                    |||||| |:|  :||
Db     126 avavpgkkkkkaaaaadhlggvvdwpppyyahnarmlaeasmatkcpegkvplisinalh 185

Qy     129 QLHVFIFVLAVFHVTYSVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSF 188
           |||:||| ||||||:|| ||:|| | |:| ||:|| |    :|:|:::|| ||||||:|||
Db     186 qlhififfflavfhvsysaitmalgrakirawkewekeaagqdyefshdptrfrfthetsf 245

Qy     189 VKRHLG-LSSTPGIRWVVAFFRQFFRSVTKVDYLTLRAGFINAHLSQNSKFDFHKYIKRS 247
           |::|:  |:  |   ::  |||||||||| : ||  ||  |:| ||:  ||||| ||||||
Db     246 vrqhmnvlnkfpasfyisnffrqffrsvrqadycalrhsfvnvhlapgskfdfqkyikrs 305

Qy     248 MEDDFKVVVGISLPLWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMAL 307
           :||||||:|||| ||| |:: |||::||  |::||| :|:||:| ||||| ||  ||:
Db     306 leddfkvivgispplwasaliflflnvngwhtmlwisimpvviilsvgtklqgiicrmai 365

Qy     308 EIQDRASVIKGAPVVEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKC 367
           :| :| :||:| |:|: |: :||| || :||| || ||||| ||: :|:| :   |:  |
Db     366 diterhaviqgipmvqvsdsyfwfarptfvlflihftlfqngfqiiyflwilyeygmdsc 425

Qy     368 YHTQIGLSIMKVVVGLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTA 427
           ::        :: :|: :| ||||:| |||||:|||| ||:||||||||||| |||  |
Db     426 fndseefvfarlclgvvvqvlcsyvtlplyalvsqmgstmkqsifdeqtskalknwraga 485

Qy     428 KEKKKVRDTDMLMAQMIGDATPSRGSSPMPSRGSS 462
           |:|          ::  |  :|: | ||  : | :
Db     486 kkkaptgg-----skhggggsptaggsptkadgda 515


RESULT  15
AAY26970
ID   AAY26970 standard; Protein; 573 AA.
XX
AC   AAY26970;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Arabidopsis thaliana fungal resistance protein CIB10295.
XX
KW   Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW   papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW   Mlo; Erysiphe graminis; powdery mildew.
XX
OS   Arabidopsis thaliana.
XX
PN   WO9947552-A2.
XX
PD   23-SEP-1999.
XX
PF   17-MAR-1999;   99WO-EP01779.
XX
PR   17-MAR-1998;   98US-0042763.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM;
XX
DR   WPI; 1999-571820/48.
DR   N-PSDB; AAZ30413.
XX
PT   New proteins useful for generating transgenic plants resistant to
PT   fungal infection  -
XX
PS   Claim 3; Page 78-81; 102pp; English.
XX
```

CC This sequence represents the Arabidopsis thaliana fungal resistance
CC protein CIB10295, which confers resistance to fungal pathogens by
CC stimulating the formation of large cell wall appositions, designated
CC papillae, at the contact site with the fungal pathogen. These papillae
CC mainly contain callose, but also contain carbohydrate, phenols and
CC proteins and are used to prevent penetration of the fungal hyphae into
CC the plant. The new Mlo sequences are used to generate transgenic plants
CC resistant to fungal pathogens, especially Erysiphe graminis (powdery
CC mildew).
XX
SQ Sequence 573 AA;

Query Match 45.0%; Score 1253.5; DB 20; Length 573;
Best Local Similarity 44.1%; Pred. No. 7.5e-127;
Matches 261; Conservative 91; Mismatches 161; Indels 79; Gaps 13;

```
Qy      1 MSDKKGVPARELPETPSWAVAVVFAAMVLVSVLMEHGLHKLGHWFQHRHKKALWEALEKM 60
          |:|:  |  | | || :||||||   :: :|:::|| :||:| ||: :||:||:|||||:
Db      1 madq--vkertleetstwavavvcfvllfisivlehsihkigtwfkkkhkqalfealekv 58

Qy     61 KAELMLVGFISLLLIVTQDPIIAKICISEDAADVMWPCKRGTEGRKPSK---------- 109
          ||||||:|||||||| : | | |: ||||:  |  | ||    | :|  |
Db     59 kaelmllgfislltigqtp-isnicisqkvastmhpcsaaeeakkygkkdagkkddgdg 117

Qy    110 --------------YV----------DYCPE-GKVALMSTGSLHQLHVFIFVLAVFHVTY 144
                        |:          | | | |||| :|   :||||:|||||||| || |
Db    118 dkpgrrlllelaesyihrrslatkgydkcaekgkvafvsaygihqlhififfvlavvhvvy 177

Qy    145 SVITIALSRLKMRTWKKWETETTSLEYQFANDPARFRFTHQTSFVKRHLGL-SSTPGIRW 203
           ::| |  ::|||||| || || ::|||::||| |||| |||  :|||  | |    |
Db    178 civtyafgkikmrtwksweeetktieyqysndperfrfardtsfgrrhlnfwsktrvtlw 237

Qy    204 VVAFFRQFFRSVTKVDYLTLRAGFINAHLS--QNSKFDFHKYIKRSMEDDFKVVVGISLP 261
          :| |||||| |||||||| || ||| || :    |:||| |||:||:| ||| || ||
Db    238 ivcffrqffgsvtkvdylalrhgfimahfapgnesrfdfrkyiqrslekdfktvveispv 297

Qy    262 LWGVAILTLFLDINGVGTLIWISFIPLVILLCVGTKLEMIIMEMALEIQDRASVIKGAPV 321
          :| ||:| |  :  |: : :|: |||||::| |||||:|| :: | ||::  |::||||
Db    298 iwfvavlflltnsyglrsylwlpfiplvvilivgtkleviitklglriqekgdvvrgapv 357

Qy    322 VEPSNKFFWFHRPDWVLFFIHLTLFQNAFQMAHFVWTVATPGLKKCYHTQIGLSIMKVVV 381
          |:| :  ||| :| ::|| ||| || ||||:| | |:     |  |:|      ::::||
Db    358 vqpgddlfwfgkprfilflihlvlftnafqlaffawstyefnlnncfhestadvvirlvv 417

Qy    382 GLALQFLCSYMTFPLYALVTQMGSNMKRSIFDEQTSKALTNWRNTAKEKKKVRDTDMLMA 441
          |  :| ||||:| |||||||||| || ::|::: : ||  | :||| : |
Db    418 gavvqilcsyvtlplyalvtqmgskmkptvfndrvatalkkwhhtaknetk-------hg 470

Qy    442 QMIGDATPSRGSSPMPSRGSSPVHLLHKGMGRSDDPQSAPTSPRTQQEARDMYPVVVAHP 501
          :  |  ||       |: ||||:|||| |   :: |:||  :            |
Db    471 rhsgsntpfssrpttpthgsspihllhnfnnrs--venypsspsprysgh-------ghh 521

Qy    502 VHRL-NPNDRRRSASSS-----ALEADIP---------------SADFSFSQ 532
           |:  :|  : : | :|     | |:  |                 ||||  :
Db    522 ehqfwdpesqhqeaetsthhslahessepvlasvelppirtskslrdfsfkk 573
```

Search completed: July 23, 2002, 14:24:34
Job time: 3432 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 09:00:27 ; Search time 1677.27 Seconds
(without alignments)
12891.259 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcggacaaaaaaggggt.....tttccttcagccagggatga 1602

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	696.8	43.5	700	10	BE519781	BE519781 HV_CEb002
c	2	583.2	36.4	669	9	AV945501	AV945501 AV945501
	3	581	36.3	605	9	AV835197	AV835197 AV835197
	4	556	34.7	798	10	BE558835	BE558835 HV_CEb002
	5	410	25.6	613	10	BE419320	BE419320 WWR06.F5R
	6	402.2	25.1	536	10	BE405266	BE405266 WHE1210_E
c	7	395.8	24.7	402	9	AV945620	AV945620 AV945620
c	8	343.2	21.4	490	10	BG904891	BG904891 TaLr1135F
	9	284.8	17.8	688	10	BI954631	BI954631 HVSMEm001
	10	253	15.8	773	10	BI808093	BI808093 C002D08 O
	11	204.6	12.8	518	10	BG904890	BG904890 TaLr1135F
	12	203.4	12.7	408	9	AV835211	AV835211 AV835211
	13	192.6	12.0	620	10	BG642916	BG642916 EST511110
	14	191	11.9	643	10	BI432930	BI432930 EST535691
	15	190.2	11.9	599	9	AW934153	AW934153 EST359996
c	16	188	11.7	663	10	BM080281	BM080281 MEST106-D
	17	185	11.5	423	10	BF729342	BF729342 1000076C0
	18	179.2	11.2	464	9	AL387000	AL387000 MtBC39D06
	19	161.2	10.1	735	10	BI931548	BI931548 EST551437
	20	158.8	9.9	615	10	BI922441	BI922441 EST542345
	21	158.8	9.9	665	10	BI923467	BI923467 EST543372
	22	152.8	9.5	598	9	BE020055	BE020055 sm38e01.y
	23	149	9.3	708	10	BG649130	BG649130 EST510749
	24	147.8	9.2	447	10	BF587392	BF587392 FM1_35_G0
c	25	145.2	9.1	545	9	BE025314	BE025314 945028C09
	26	145.2	9.1	761	10	BG130233	BG130233 EST475879
	27	143	8.9	707	10	BM410789	BM410789 EST585116
	28	137.8	8.6	576	9	AI993856	AI993856 701515174
	29	137.2	8.6	849	10	BI309518	BI309518 EST530928
	30	134.4	8.4	440	10	BF096305	BF096305 EST360354
	31	133	8.3	605	9	AW216578	AW216578 EST295292
	32	131.8	8.2	636	10	BM359705	BM359705 GA__Ea002
	33	131.4	8.2	622	9	AI729603	AI729603 BNLGHi137
	34	131.2	8.2	628	9	AI729043	AI729043 BNLGHi124
	35	130.8	8.2	471	10	BE636983	BE636983 WHE1808_C
	36	129	8.1	622	9	AI731933	AI731933 BNLGH1114
	37	126.8	7.9	585	10	N37544	N37544 18771 Lambd
	38	122.6	7.7	523	10	BI126403	BI126403 I075P03P
	39	120	7.5	410	10	BM409501	BM409501 EST583828
	40	119.8	7.5	456	10	BG132655	BG132655 EST465547
	41	116.8	7.3	569	10	BE354015	BE354015 EST355358
	42	116.2	7.3	456	9	AW132264	AW132264 sd98f11.y
	43	114.6	7.2	394	9	AV536614	AV536614 AV536614
	44	114.2	7.1	447	9	AW132268	AW132268 sd98g11.y
c	45	112.2	7.0	688	9	AV836759	AV836759 AV836759

ALIGNMENTS

RESULT 1
BE519781
LOCUS BE519781 700 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEb0021D05f Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone HV_CEb0021D05f, mRNA sequence.
ACCESSION BE519781
VERSION BE519781.2 GI:13266203
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 700)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi ,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library
JOURNAL Unpublished (2001)
COMMENT On Aug 8, 2000 this sequence version replaced gi:9743969.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 586
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence start: 4
High quality sequence stop: 664.
FEATURES Location/Qualifiers
source 1. .700
/organism="Hordeum vulgare"
/cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
/clone="HV_CEb0021D05f"

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                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0005 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16151 (Mla6) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate 5874 (AvrMla6
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids (Choi, Close). Phagemids were plated and picked
                     at the Clemson University Genomics Institute (CUGI) (Begum
                     , Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      149 a    210 c    191 g    150 t
ORIGIN

  Query Match           43.5%;  Score 696.8;  DB 10;  Length 700;
  Best Local Similarity  99.7%;  Pred. No. 1.4e-124;
  Matches  698;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy    280 gtcatgtggccctgcaagcgcggcaccgagggccgcaagcccagcaagtacgttgactac 339
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GTCATGTGGCCCTGCAAGCGCGGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTAC 60

Qy    340 tgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgtcttc 399
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 TGCCCGGAGGGCAAGGTGGCGCTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTC 120

Qy    400 atcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaagccgt 459
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 ATCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGT 180

Qy    460 ctcaaaatgagaacatggaagaaatgggagacagagaccacctccttggaataccagttc 519
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCACCTCCTTGGAATACCAGTTC 240

Qy    520 gcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcgccacctg 579
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GCAAATGATCCTGCACGGTTCCGGTTCACGCACCAGACGTCGTTCGTGAAGCGCCACCTG 300

Qy    580 ggcctctccagcacccctggcatcagatgggtggtggccttcttcaggcagttcttcagg 639
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GGCCTCTCCAGCACCCCTGGCATCAGATGGGTGGTGGCCTTCTTCAGGCAGTTCTTCAGG 360

Qy    640 tcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcg 699
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TCAGTCACCAAGGTGGACTACCTGACCTTGAGGGCAGGCTTCATCAACGCGCATTTGTCG 420

Qy    700 caaaacagcaagttcgacttccacaagtacatcaagaggtcgatggaggacgacttcaag 759
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CAAAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTCGATGGAGGACGACTTCAAG 480

Qy    760 gtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgac 819
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GTCGTCGTCGGCATCAGCCTCCCGCTGTGGGGTGTGGCGATCCTCACCCTCTTCCTTGAC 540

Qy    820 atcaatggggttggcacgctcatctggatttctttcatccctctcgtgatcctcttgtgt 879
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 ATCAATGGGGTTGGCACGCTCATCTGGATTTCTTTCATCCCTCTCGTGATCCTCTTGTGT 600

Qy    880 gttggaaccaagctggagatgatcatcatggagatggccctggagatccaggaccgggcg 939
          ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    601 GTTGGAACCAAGCTGGAGATGATCATCATGGAGATGGCCCTGGAGATCCAAGACCGGGCG 660

Qy    940 agcgtcatcaaggggccccccgtggtcgagcccagcaaca 979
          |||||||||||||||||||||||||| ||||||||||||
Db    661 AGCGTCATCAAGGGGGCCCCCGTGGTCCAGCCCAGCAACA 700


RESULT   2
AV945501/c
LOCUS       AV945501                669 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV945501 K. Sato unpublished cDNA library, strain H602 adult,
            heading stage top three leaves Hordeum vulgare subsp. spontaneum
            cDNA clone bah26o13 3', mRNA sequence.
ACCESSION   AV945501
VERSION     AV945501.1  GI:18241298
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah26o13"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT      131 a    182 c    192 g    163 t      1 others
ORIGIN

  Query Match           36.4%;  Score 583.2;  DB 9;  Length 669;
  Best Local Similarity  99.5%;  Pred. No. 1.1e-102;
  Matches  585;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy   1015 ttcttcatacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggaca 1074
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    669 TTCTTCATACACCTGACGTTGTTCCAGAACGCGTTTCAGATGGCGCATTTTGTGTGGACA 610

Qy   1075 gtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaag 1134
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    609 GTGGCCACGCCCGGCTTGAAGAAATGCTACCACACGCAGATCGGGCTGAGCATCATGAAG 550

Qy   1135 gtggtggtggggctagctctccagttcctctgcagctatatgaccttcccccctctacgcg 1194
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    549 GTGGTCGTGGGGCTAGCTCTCCAGTTCCTCTGCAGCTATATGACCTTCCCCCTCTACGCG 490

Qy   1195 ctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaag 1254
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Db    489 CTCGTCACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAG 430

Qy   1255 gcgctcaccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatg 1314
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    429 GCGCTCACCAACTGGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATG 370

Qy   1315 ctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagc 1374
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    369 CTGATGGCTCAGATGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGC 310

Qy   1375 cggggctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccag 1434
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    309 CGGGGCTCATCACCCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAG 250

Qy   1435 agcgcgcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtg 1494
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    249 AGCGCGCCCACCTCGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTG 190

Qy   1495 gcgcacccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggcc 1554
          |||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Db    189 GCGCACCCGGTGCACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCATCATCGGCC 130

Qy   1555 ctcgaagccgacatccccagtgcagatttttccttcagccagggatga 1602
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db    129 CTCGAAGCCGACATCCCCAGTGCAGATTTTTCCTTCAGCCAGGGATGA 82
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RESULT 3
AV835197
LOCUS AV835197 605 bp mRNA linear EST 22-JUN-2001
DEFINITION AV835197 K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage Hordeum vulgare subsp. spontaneum cDNA clone bah26o13, mRNA sequence.
ACCESSION AV835197
VERSION AV835197.1 GI:14527286
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. spontaneum.
ORGANISM Hordeum vulgare subsp. spontaneum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 605)
AUTHORS Sato,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2001)
COMMENT Contact: Kazuhiro Sato
Research Institute for Bioresources
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazsato@rib.okayama-u.ac.jp,
URL:http://www.rib.okayama-u.ac.jp/barley/
Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct submission;
database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES Location/Qualifiers
source 1. .605
/organism="Hordeum vulgare subsp. spontaneum"
/cultivar="H602"
/db_xref="taxon:77009"
/clone="bah26o13"
/clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. spontaneum top three leaves adult, heading stage"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
BASE COUNT 131 a 188 c 163 g 122 t 1 others
ORIGIN

Query Match 36.3%; Score 581; DB 9; Length 605;
Best Local Similarity 99.8%; Pred. No. 3e-102;
Matches 592; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy    214 ctgctcctcatcgtcacgcagg-accccatcatcgccaagatatgcatctccgaggatgc 272
          ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db     13 CTGCTCCTCATCGTCACGCAGGNACCCCATCATCGCCAAGATATGCATCTCCGAGGATGC 72

Qy    273 cgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccagcaagtacgt 332
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     73 CGCCGACGTCATGTGGCCCTGCAAGCGCGGCACCGAGGGCCGCAAGCCCAGCAAGTACGT 132

Qy    333 tgactactgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctgca 392
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    133 TGACTACTGCCCGGAGGGCAAGGTGGCGCTCATGTCCACGGGCAGCTTGCACCAGCTGCA 192

Qy    393 cgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagctct 452
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    193 CGTCTTCATCTTCGTGCTCGCGGTCTTCCATGTCACCTACAGCGTCATCACCATAGCTCT 252

Qy    453 aagccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctccttggaata 512
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    253 AAGCCGTCTCAAAATGAGAACATGGAAGAAATGGGAGACAGAGACCACCTCCTTGGAATA 312

Qy    513 ccagttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcg 572
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 CCAGTTCGCAAATGATCCTGCACGGTTCCGGTTCACGCACCAGACGTCGTTCGTGAAGCG 372

Qy    573 ccacctgggcctctccagcacccctggcatcagatgggtggtggccttcttcaggcagtt 632
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    373 CCACCTGGGCCTCTCCAGCACCCCTGGCATCAGATGGGTGGTGGCCTTCTTCAGGCAGTT 432

Qy    633 cttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgca 692
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    433 CTTCAGGTCAGTCACCAAGGTGGACTACCTGACCTTGAGGGCAGGCTTCATCAACGCGCA 492

Qy    693 tttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcgatggaggacga 752
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    493 TTTGTCGCAAAACAGCAAGTTCGACTTCCACAAGTACATCAAGAGGTCGATGGAGGACGA 552

Qy    753 cttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctca 805
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    553 CTTCAAGGTCGTCGTCGGCATCAGCCTCCCGCTGTGGGGTGTGGCGATCCTCA 605
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RESULT 4
BE558835
LOCUS BE558835 798 bp mRNA linear EST 23-OCT-2001
DEFINITION HV_CEb0020I08f Hordeum vulgare seedling green leaf EST library HVcDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone HV_CEb0020I08f, mRNA sequence.
ACCESSION BE558835
VERSION BE558835.3 GI:16336267
KEYWORDS EST.
SOURCE barley.
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae ; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 798)
AUTHORS Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi ,D.W., Fenton,R.D., Oates,R. and Main,D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedling leaf cDNA library
JOURNAL Unpublished (2001)
COMMENT On Aug 14, 2000 this sequence version replaced gi:13266126.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 458
Seq primer: AATTAACCCTCACTAAAGGG

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          High quality sequence stop: 561.
FEATURES             Location/Qualifiers
     source          1. .798
                     /organism="Hordeum vulgare"
                     /cultivar="CI16151 (Mla6)"
                     /db_xref="taxon:4513"
                     /clone="HV_CEb0020I08f"
                     /clone_lib="Hordeum vulgare seedling green leaf EST
                     library HVcDNA0005 (Blumeria challenged)"
                     /tissue_type="seedling green leaf"
                     /lab_host="SOLR"
                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
                     C.I. 16151 (Mla6) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were challenged with isolate 5874 (AvrMla6
                     ) of Blumeria graminis f. sp. hordei, and leaves were
                     harvested 20 and 24 hr post-inoculation and snap frozen;
                     uninoculated leaves were harvested 20 hr post-inoculation
                     (Wei, Wise). In the TJ Close lab at the University of
                     California, Riverside, total RNA was prepared from each
                     sample pool, equal quantities of all three RNA pools were
                     combined, poly(A) RNA was purified from the mixture, one
                     primary unamplified cDNA library was made, and 1 million
                     pfu were in vivo excised to give pBluescript SK(-) cDNA
                     phagemids (Choi, Close). Phagemids were plated and picked
                     at the Clemson University Genomics Institute (CUGI) (Begum
                     , Palmer, Frisch, Atkins and Wing). Plasmid DNA
                     preparations, DNA sequencing and sequence analysis were
                     performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates
                     , Rambo, Main). The sequence has been trimmed to remove
                     vector sequence and contains a minimum of 100 bases of
                     phred value 20 or above. For more details on library
                     preparation and sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT       153 a    244 c    241 g    158 t      2 others
ORIGIN
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  Query Match             34.7%;  Score 556;  DB 10;  Length 798;
  Best Local Similarity   96.2%;  Pred. No. 2.1e-97;
  Matches  579;  Conservative    0;  Mismatches   22;  Indels    1;  Gaps    1;

Qy       1 atgtcggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     197 ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG 256

Qy      61 gcggtggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaag 120
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     257 GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAGCACGGCCTCCACAAG 316

Qy     121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     317 CTCGGCCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG 376

Qy     181 aaggcggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggacccc 240
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     377 AAGGCGGAGCTCATGCTGGTGGGCTTCATATCCCTGCTCCTCATCGTCACGCAGGACCCC 436

Qy     241 atcatcgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgc 300
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     437 ATCATCGCCAAGATATGCATCTCCGAGGATGCCGCCGACGTCATGTGGCCCTGCAAGCGC 496

Qy     301 ggcaccgagggccgcaagcccagcaagtacgttgactactgcccggagggcaaggtggcg 360
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     497 GGCACCGAGGGCCGCAAGCCCAGCAAGTACGTTGACTACTGCCCGGAGGGCAAGGTGGCG 556

Qy     361 ctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttc 420
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Db     557 CTCATGTCCACGGGCAGCTTGCACCAGCTGCACGTCTTCATCTTCGTGCTCGCGGTCTTC 616

Qy     421 catgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaag 480
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     617 CATGTCACCTACAGCGTCATCACCATAGCTCTAAGCCGTCTCAAAATGAGAACATGGAAG 676

Qy     481 aaatgggagacagagaccacctccttgg-aataccagttcgcaaatgatcctgcacggtt 539
           |||||||||||||||||||||| ||||| ||||||| |||||||||||||||||||||| |
Db     677 AAATGGGAGACAGAGACCACCTNCTTGGAAATACCAATTCGCAAATGATCCTGCACGGGT 736

Qy     540 ccggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctgg 599
           ||||||||||||||| |||||| |     ||||||| ||| | || | ||  | |||| |
Db     737 NCGGTTCACGCACCAAACGTCGGTTCGTGAGCGCCAACTGTGGCTTTTCAAGAACCCTTG 796

Qy     600 ca 601
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Db     797 GA 798
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RESULT   5
BE419320
LOCUS       BE419320                613 bp    mRNA    linear   EST 24-JUL-2000
DEFINITION  WWR06.F5R000101 ITEC WWR Wheat Root Library Triticum aestivum cDNA
            clone WWR06.F5, mRNA sequence.
ACCESSION   BE419320
VERSION     BE419320.1  GI:9417166
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 613)
  AUTHORS   Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
            ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
            Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
            Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
            Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
            Sorrells,M., Warburton,M. and Wenzel,G.
  TITLE     International Triticeae EST Cooperative (ITEC): Production of
            Expressed Sequence Tags for Species of the Triticeae
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Schuch W
            Zeneca Wheat Improvement Centre, Norwich Research Park
            Colney Lane, Norwich NR4 7UH UNITED KINGDOM
            Tel: 44 1603 250 2600
            Fax: 44 1603 250 699
            Email: wolfgang.schuch@aguk.zeneca.com
            International Triticeae EST Cooperative (ITEC)
            http://wheat.pw.usda.gov/genome.
FEATURES             Location/Qualifiers
     source          1. .613
                     /organism="Triticum aestivum"
                     /cultivar="Novosibirskaya 67"
                     /db_xref="taxon:4565"
                     /clone="WWR06.F5"
                     /clone_lib="ITEC WWR Wheat Root Library"
                     /tissue_type="root"
                     /note="M13 Reverse sequencing primer used for 5' end of
                     clone. "
BASE COUNT       121 a    180 c    150 g    159 t      3 others
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  Query Match             25.6%;  Score 410;  DB 10;  Length 613;
  Best Local Similarity   91.9%;  Pred. No. 2.9e-69;
  Matches  442;  Conservative    0;  Mismatches   38;  Indels    1;  Gaps    1;

Qy     774 cagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttgg 833
           |||||||||||||||| |||||||||||| |||||||||||||| ||| |  || | ||
Db     133 CAGCCTCCCGCTGTGGGCTGTGGCGATCCTNACCCTCTTCCTTGATATCNACNGGATCGG 192

Qy     834 cacgctcatctggatttct-ttcatccctctcgtgatcctcttgtgtgttggaaccaagc 892
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Db    193 CACACTCACCTGGGTTGATCATCATCCCTCTCATCATCCTCTTGTGTGTTGGAACCAAGC 252

Qy    893 tggagatgatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaagg 952
          | ||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db    253 TAGAGATGATCATCATGGAGATGGCCCTGGAGATCCAGGACCGGTCGAGCGTCATCAAGG 312

Qy    953 gggcccccgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcc 1012
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    313 GGGCACCCGTGGTCGAGCCCAGCAACAAGTTCTTCTGGTTCCACCGCCCCGACTGGGTCC 372

Qy   1013 tcttcttcatacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtgga 1072
          |||||||||||||||||||| |||||||||||||||||||||||||| ||||| |||||||
Db    373 TCTTCTTCATACACCTGACGCTGTTCCAGAACGCGTTTCAGATGGCACATTTCGTGTGGA 432

Qy   1073 cagtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatga 1132
          |||||||||||||||||||| | |||| ||| | | | ||||||||||||||||||||
Db    433 CAGTGGCCACGCCCGGCTTGAAGGACTGCTTCCATATGAACATCGGGCTGAGCATCATGA 492

Qy   1133 aggtggtggtggggctagctctccagttcctctgcagctatatgaccttccccctctacg 1192
          |||| ||| |||||||| |||||||||||||| |||||||| || ||||||||||||||||
Db    493 AGGTCGTGCTGGGGCTGGCTCTCCAGTTCCTGTGCAGCTACATCACCTTCCCCCTCTACG 552

Qy   1193 cgctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtcca 1252
          |||| ||||||||||||||||||||||||||||||||||||||||||||||||||  |||
Db    553 CGCTAGTCACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACAGCCA 612

Qy   1253 a 1253
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Db    613 A 613
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RESULT   6
BE405266
LOCUS       BE405266                 536 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  WHE1210_E11_I22ZS Wheat etiolated seedling root cDNA library
            Triticum aestivum cDNA clone WHE1210_E11_I22, mRNA sequence.
ACCESSION   BE405266
VERSION     BE405266.1  GI:9364734
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Strategene SK primer.
FEATURES             Location/Qualifiers
     source          1. .536
                     /organism="Triticum aestivum"
                     /cultivar="Chinese Spring"
                     /db_xref="taxon:4565"
                     /clone="WHE1210_E11_I22"
                     /clone_lib="Wheat etiolated seedling root cDNA library"
                     /tissue_type="Root"
                     /dev_stage="Five day old etiolated seedling"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
                     , germinated and grown aseptically in the  dark at room
                     temperature on filter paper with water, nystatin and
                     cefotaxime in covered crystallization dishes. Roots were
                     harvested.  The tissue, total RNA, and poly(A) RNA were
                     prepared, a cDNA library  was made, and the cDNA clones
                     were in vivo excised to give pBluescript  phagemids in the
                     TJ Close lab (Choi, Close, Fenton) at the University  of
                     California, Riverside.  Plasmid DNA preparations and DNA
                     sequencing  were performed in the OD Anderson lab (all
                     other authors)."
BASE COUNT      117 a    173 c    136 g    110 t
ORIGIN
```

```
  Query Match             25.1%;  Score 402.2;  DB 10;  Length 536;
  Best Local Similarity   87.9%;  Pred. No. 8.9e-68;
  Matches  474;  Conservative    0;  Mismatches   58;  Indels    7;  Gaps    3;

Qy    201 gggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcat 260
          ||||||||| || ||||| |||  ||| |||||||||||||||  ||    |||||||||
Db      1 GGGCTTCATCTCGCTGCTGCTCGCCGTGACGCAGGACCCCATCTCCGG---GATATGCAT 57

Qy    261 ctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcc 320
          ||||||| | ||||||  | ||||| ||||||||||||    | | |.   |  ||||
Db     58 CTCCGAGAAGGCCGCCAGCATCATGCGGCCCTGCAAGCTGCCCCCTGGCTCCGTCAAGAG 117

Qy    321 cagcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcag 377
          ||   |  | |   |||||||| |     |||||||||| ||||||||||||||||||
Db    118 CAAGTACAAAGACTACTACTGCGCCAAACAGGGCAAGGTGTCGCTCATGTCCACGGGCAG 177

Qy    378 cttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgt 437
          |||||||||||||||| | |||||||||||||||| ||||||||||||||||||||||||
Db    178 CTTGCACCAGCTGCACATATTCATCTTCGTGCTCGCCGTCTTCCATGTCACCTACAGCGT 237

Qy    438 catcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagac 497
          ||||| ||| ||||||||||||||||||||||||| ||||||||||||||||||||||||
Db    238 CATCATCATGGCTCTAAGCCGTCTCAAAATGAGAACCTGGAAGAAATGGGAGACAGAGAC 297

Qy    498 cacctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagac 557
          | ||||| |||||||||||||||||||||||||||||| |||||||| ||||||||||||
Db    298 CGCCTCCCTGGAATACCAGTTCGCAAATGATCCTGCGCGGTTCCGCTTCACGCACCAGAC 357

Qy    558 gtcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatgggt-ggtgg 616
          |||||||||||||| |||||||||||||||||||||| ||| |||||||||| |||||
Db    358 GTCGTTCGTGAAGCGGCACCTGGGCCTCTCCAGCACCCCCGGCGTCAGATGGGTGGGTGG 417

Qy    617 ccttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcag 676
          |||||||||||||||||||||| |||||||||||||||||||| ||||||||||||||||
Db    418 CCTTCTTCAGGCAGTTCTTCAGGTCGGTCACCAAGGTGGACTACCTCACCTTGAGGGCAG 477

Qy    677 gcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaag 735
          |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db    478 GCTTCATCAACGCGCATTTGTCGCATAACAGCAAGTTCGACTTCCACAAGTACATCAAG 536
```

```
RESULT   7
AV945620/c
LOCUS       AV945620                 402 bp    mRNA    linear   EST 18-JAN-2002
DEFINITION  AV945620 K. Sato unpublished cDNA library, strain H602 adult,
            heading stage top three leaves Hordeum vulgare subsp. spontaneum
            cDNA clone bah27g01 3', mRNA sequence.
ACCESSION   AV945620
VERSION     AV945620.1  GI:18241417
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Sato,K., Saisho,D. and Takeda,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
```

```
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tshini@genes.nig.ac.jp.
FEATURES             Location/Qualifiers
     source          1. .402
                     /organism="Hordeum vulgare subsp. spontaneum"
                     /strain="H602"
                     /db_xref="taxon:77009"
                     /clone="bah27g01"
                     /clone_lib="K. Sato unpublished cDNA library, strain H602
                     adult, heading stage top three leaves"
                     /tissue_type="top three leaves"
                     /dev_stage="adult, heading stage"
BASE COUNT       60 a    116 c    127 g     96 t      3 others
ORIGIN

  Query Match             24.7%;  Score 395.8;  DB 9;  Length 402;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-66;
  Matches  397;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy   1148 tagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcacacaga 1207
          ||||||||||||||| | |||||||||||||||||||||| ||||||||||||||||||
Db    402 TAGCTCTCCAGTTCNTNTGCAGCTATATGACCTTCCCCCTNTACGCGCTCGTCACACAGA 343

Qy   1208 tgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaact 1267
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    342 TGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGTCCAAGGCGCTCACCAACT 283

Qy   1268 ggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatggctcaga 1327
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    282 GGCGGAACACGGCCAAGGAGAAGAAGAAAGTCCGAGACACGGACATGCTGATGGCTCAGA 223

Qy   1328 tgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggctcatcac 1387
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    222 TGATCGGCGACGCAACACCGAGCCGAGGCTCGTCGCCGATGCCGAGCCGGGGCTCATCAC 163

Qy   1388 ccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgcccacct 1447
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    162 CCGTGCACCTGCTTCACAAGGGCATGGGGCGGTCGGACGACCCCCAGAGCGCGCCCACCT 103

Qy   1448 cgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgc 1507
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    102 CGCCAAGGACCCAGCAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGCACCCGGTGC 43

Qy   1508 acagactaaatcctaacgacaggaggaggtccgcctcgtcgt 1549
          |||||||||||||||||||||||||||||||||| || | |
Db     42 ACAGACTAAATCCTAACGACAGGAGGAGGTCCGCCTCATCAT 1


RESULT   8
BG904891/c
LOCUS       BG904891                490 bp    mRNA    linear   EST 05-JUN-2001
DEFINITION  TaLr1135F04F TaLr1 Triticum aestivum cDNA clone TaLr1135F04 3',
            mRNA sequence.
ACCESSION   BG904891
VERSION     BG904891.1  GI:14312567
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Cloutier,S., Dong,G. and Walsh,A.
  TITLE     Wheat functional genomics- Thatcher Lr1 cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dr. Sylvie Cloutier
            Cereal Research Centre, Agriculture and Agri-food Canada
            195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
            Tel: (204) 983-2340
            Fax: (204) 983-4604
            Email: scloutier@em.agr.ca
            was cloned directionally, not all sequences generated with reverse
            primer were from the 5' end (same with forward primer and 3' end).
            Average inset size is >2.2 kb
            Plate: 135  row: F  column: 04
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Triticum aestivum"
                     /cultivar="Thatcher Lr1"
                     /db_xref="taxon:4565"
                     /clone="TaLr1135F04"
                     /clone_lib="TaLr1"
                     /tissue_type="Leaf tissue"
                     /dev_stage="14 Days old"
                     /lab_host="E. coli XLOLR"
                     /note="Vector: Lambda ZapII; mass excised in plasmid
                     vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
                     mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
                     inoculation  with leaf rust pathogen Puccinia triticina
                     race BBB carrying the  avirulence gene Avr1."
BASE COUNT       90 a    143 c    130 g    127 t
ORIGIN

  Query Match             21.4%;  Score 343.2;  DB 10;  Length 490;
  Best Local Similarity   90.6%;  Pred. No. 2.1e-56;
  Matches  366;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy   1199 tcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgc 1258
          ||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db    490 TCACACAGATGGGATCAAACATGAAGAGGTCCATCTTCGACGAGCAGACGGCCAAGGCGC 431

Qy   1259 tcaccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctga 1318
          | || |||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db    430 TGACAAACTGGCGGAACACGGCCAAGGAGAAGAAGAAGGTCCGAGACACGGACATGCTGA 371

Qy   1319 tggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggg 1378
          |||| |||||||||||||||| || || ||||||||  ||||||| ||||| |||||||
Db    370 TGGCGCAGATGATCGGCGACGCGACGCCCAGCCGAGGGGCGTCGCCCATGCCTAGCCGGG 311

Qy   1379 gctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcg 1438
          |||| || || |||||||||||||||||||||||||||| ||||| ||||| |||||||||
Db    310 GCTCGTCGCCAGTGCACCTGCTTCACAAGGGCATGGGACGGTCCGACGATCCCCAGAGCA 251

Qy   1439 cgcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgc 1498
          |||| |||||||||||| ||  | ||||||||||||||||||||||||||||||||||||
Db    250 CGCCAACCTCGCCAAGGGCCATGGAGGAGGCTAGGGACATGTACCCGGTTGTGGTGGCGC 191

Qy   1499 acccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcg 1558
          | || |||||||||||||||||   |||||||| ||||| | ||||||||||||| ||||
Db    190 ATCCAGTGCACAGACTAAATCCTGCTGACAGGAGAAGGTCGGTCTCGTCGTCGGCACTCG 131

Qy   1559 aagccgacatccccagtgcagatttttccttcagccagggatga 1602
          | | |||||| ||||| |||||||||||||||||||| ||||||
Db    130 ATGTCGACATTCCCAGCGCAGATTTTTCCTTCAGCCAAGGATGA 87


RESULT   9
BI954631
LOCUS       BI954631                688 bp    mRNA    linear   EST 19-OCT-2001
DEFINITION  HVSMEm0018P07f Hordeum vulgare green seedling EST library
            HVcDNA0014 (Blumeria infected) Hordeum vulgare cDNA clone
            HVSMEm0018P07f, mRNA sequence.
ACCESSION   BI954631
VERSION     BI954631.1  GI:16300302
KEYWORDS    EST.
SOURCE      barley.
  ORGANISM  Hordeum vulgare
```

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           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
           ; Triticeae; Hordeum.
REFERENCE  1  (bases 1 to 688)
  AUTHORS  Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
           Frisch,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons
           ,J., Oates,R. and Main,D.
  TITLE    Development of a genetically and physically anchored EST resource
           for barley genomics: Blumeria infected Morex (compatible) seedling
           cDNA library
  JOURNAL  Unpublished (2001)
COMMENT    Contact: Wing RA
           Clemson University Genomics Institute
           Clemson University
           100 Jordan Hall, Clemson, SC 29634, USA
           Tel: 864 656 7288
           Fax: 864 656 4293
           Email: rwing@clemson.edu
           Total hq bases = 236
           Seq primer: AATTAACCCTCACTAAAGGG
           High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .688
                     /organism="Hordeum vulgare"
                     /cultivar="Morex"
                     /db_xref="taxon:4513"
                     /clone="HVSMEm0018P07f"
                     /clone_lib="Hordeum vulgare green seedling EST library
                     HVcDNA0014 (Blumeria infected)"
                     /tissue_type="green seedling leaf"
                     /lab_host="TJC121"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Morex (mla) plants were greenhouse grown in the R
                     Wise lab at Iowa State University, Ames, IA; 7 day old
                     green seedlings were infected with isolate 5874 of
                     Blumeria graminis f. sp. hordei, and leaves were harvested
                     24, 48 and 72 hr post-inoculation and snap frozen (Wise).
                     In the TJ Close lab at the University of California,
                     Riverside, total RNA was prepared from each sample pool,
                     equal quantities of all three RNA pools were combined,
                     poly(A) RNA was purified from the mixture, one primary
                     unamplified cDNA library was made, and 1 million pfu were
                     in vivo excised to give pBluescript SK(-) cDNA phagemids
                     (Chin). Phagemids were plated and picked at the Clemson
                     University Genomics Institute (CUGI) (Begum, Palmer,
                     Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
                     sequencing and sequence analysis were performed at CUGI
                     (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                     The sequence has been trimmed to remove vector sequence
                     and contains a minimum of 100 bases of phred value 20 or
                     above. For more details on library preparation and
                     sequence analysis see
                     http://www.genome.clemson.edu/projects/barley. To order
                     this clone see http://www.genome.clemson.edu/orders Also
                     see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
                     Genetically and physically anchored EST resources for
                     barley genomics. Barley Genetics Newsletter 31:29-30.
                     (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)"
BASE COUNT      129 a    185 c    258 g    113 t      3 others
ORIGIN
```

```
  Query Match             17.8%;  Score 284.8;  DB 10;  Length 688;
  Best Local Similarity   83.2%;  Pred. No. 4.1e-45;
  Matches  347;  Conservative    0;  Mismatches   68;  Indels    2;  Gaps    2;

Qy       1 atgtcggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtg 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     210 ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG 269

Qy      61 gcggtggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaag 120
           |||||||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Db     270 GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAGCACGGACTCCACAAG 329

Qy     121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
           ||||| ||||||||||||||||||||||||||||||||||||||||||||||| || |||
Db     330 CTCGGACATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGACAAAATG 389

Qy     181 aaggcggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggacccc 240
           |||||||||||||||||| |||||| |||| |||||||||| ||||||||||||| ||
Db     390 AAGGCGGAGCTCATGCTGGCGGGCTTAATATGCCTGCTCCTAATCGTCACGCAGGAACCG 449

Qy     241 atcatcgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgc 300
           |||||||||| |||||||||||||||||| ||| ||||  || || |||||||| || |
Db     450 ATCATCGCCAAAATATGCATCTCCGAGGATCCCGGCGACAGCAAGTAGCCCTGCAGGCAC 509

Qy     301 -ggcaccgagggccgcaagcccagcaagtacgttgactact-gcccggagggcaaggtgg 358
            |||    ||||||  | | | |  ||  ||||||||  || ||| || ||||| || ||
Db     510 GGGCGTGAAGGGCCCGAGGGCGATGAAAGACGTTGACAGCTGGCCGGGGGGGCATGGAGG 569

Qy     359 cgctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcgg 415
             |    ||  ||| ||   | || | |||| ||    |  |  |  | ||| | ||
Db     570 GACCACGGTTAACGAGCGNTTAGCGCGAGCTACAGCGATATAGGTCAGAGCTAGGGG 626
```

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RESULT  10
BI808093
LOCUS       BI808093                773 bp    mRNA    linear   EST 02-OCT-2001
DEFINITION  C002D08 Oryza sativa mature leaf library induced by M.grisea Oryza
            sativa cDNA clone C002D08, mRNA sequence.
ACCESSION   BI808093
VERSION     BI808093.1  GI:15855281
KEYWORDS    EST.
SOURCE      Oryza sativa.
  ORGANISM  Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 773)
  AUTHORS   Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
            ,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
  TITLE     A Gene Expression Screen in Oryza sativa
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dong HT
            Laboratory of Functional Genetics
            Bio-technology Institute of Zhejiang University
            Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
            Tel: 0086-571-86892051
            Fax: 0086-571-86961525
            Email: htdong@zjuem.zju.edu.cn
            Seq primer: M13 forward primer.
FEATURES              Location/Qualifiers
     source           1. .773
                      /organism="Oryza sativa"
                      /db_xref="taxon:4530"
                      /clone="C002D08"
                      /clone_lib="Oryza sativa mature leaf library induced by
                      M.grisea"
                      /tissue_type="leaf"
                      /dev_stage="Mature stage"
                      /note="Vector: pSport2"
BASE COUNT      178 a    209 c    217 g    169 t
ORIGIN
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  Query Match             15.8%;  Score 253;  DB 10;  Length 773;
  Best Local Similarity   67.3%;  Pred. No. 5.7e-39;
  Matches  445;  Conservative    0;  Mismatches  185;  Indels   31;  Gaps    5;

Qy     838 ctcatctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggag 897
           | || |  || |  ||| |   |  | |      | | |  |||| |      | ||||||
Db      63 CGCACCCTTATCTGATTCGTGTGTGCCACTCGTCACCTCAGTGTGGTTGGACAACTGGAG 122

Qy     898 atgatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcc 957
           ||  | ||||||||| | | | ||||||||| ||  |||    || ||||||| ||
Db     123 ATTGTTATCATGGAGA-GCCACAGGAGATCCAGAACACGGCACTGGTGATCAAGGGAGCA 181
```

```
Qy    958 cccgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttc 1017
          |    | |||    |    |||||| ||||| |||  |||| || || |||||| | |||
Db    182 C----GTTCGTTAACCAACACAAGTACTTCT-GTTTAACCGGCCTGATTGGGTCTTGTTC 236

Qy   1018 ttcatacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtg 1077
          ||||||    ||         | |   |||| |||||||||||| ||||| ||||||||  ||
Db    237 TTCATGACACTTGATACTGTTCCAGACGCATTTCAGATGGCACATTTCGTGTGGACTCTG 296

Qy   1078 gccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtg 1137
          || || |  | ||  |  ||    | |||     | || ||  |||| |||||||| ||
Db    297 GCAACCCTGGCCTGAAGAAATGCGTTCCATGAAAACATGGGCTTGAGTATCATGAAAGTT 356

Qy   1138 gtggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctc 1197
          || |||||| ||    | |||||||| |||||||| |  |||||||| |||||||| |||
Db    357 GTAGTGGGGATATTCATTCAGTTCCTATGCAGCTACAGCACCTTCCCTCTCTACGCACTC 416

Qy   1198 gtcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcg 1257
          ||||||||||||||||||||||||| | ||||||||||  |||||||||   |||||
Db    417 GTCACACAGATGGGATCAAACATGAAGAAGACCATCTTCGAGGAGCAGACGATGAAGGCC 476

Qy   1258 ctcaccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctg 1317
          || |  |||||| |||| ||||| | ||||||||||||  |||| ||| | |||  | |
Db    477 CTGATGAACTGGAGGAAGACGGCGAGGGAGAAGAAGAAGCTCCGGGACGCCGACGAGTTC 536

Qy   1318 atggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccgg 1377
           | || ||||||| ||||||| | || |||||||| ||||||||||||
Db    537 CTAGCACAGATGA-CGGCGACACGACGCCGAGCCGCGGCTCGTCGCCG------------ 583

Qy   1378 ggctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagc 1437
                    ||||||||||| ||||||   | || | ||||||| || || | ||||
Db    584 ------------GTGCACCTGCTGCACAAGCAAAGGGTGAGGTCGGAAGATCCGCCGAGC 631

Qy   1438 gcgcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcg 1497
          || ||  | |||||  ||  |      |||||| |||||||||||||||||    ||||||
Db    632 GCACCGGCATCGCCGGGGTTCGCCGGAGAGGCCAGGGACATGTACCCGGTGCCCGTGGCG 691

Qy   1498 c 1498
          |
Db    692 C 692
```

```
RESULT  11
BG904890
LOCUS       BG904890                518 bp    mRNA    linear   EST 05-JUN-2001
DEFINITION  TaLr1135F04R TaLr1 Triticum aestivum cDNA clone TaLr1135F04 5',
            mRNA sequence.
ACCESSION   BG904890
VERSION     BG904890.1  GI:14312566
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 518)
  AUTHORS   Cloutier,S., Dong,G. and Walsh,A.
  TITLE     Wheat functional genomics- Thatcher Lr1 cDNA library
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Dr. Sylvie Cloutier
            Cereal Research Centre, Agriculture and Agri-food Canada
            195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
            Tel: (204) 983-2340
            Fax: (204) 983-4604
            Email: scloutier@em.agr.ca
            was cloned directionally, not all sequences generated with reverse
            primer were from the 5' end (same with forward primer and 3' end).
            Average inset size is >2.2 kb
            Plate: 135  row: F  column: 04
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .518
                     /organism="Triticum aestivum"
                     /cultivar="Thatcher Lr1"
                     /db_xref="taxon:4565"
                     /clone="TaLr1135F04"
                     /clone_lib="TaLr1"
                     /tissue_type="Leaf tissue"
                     /dev_stage="14 Days old"
                     /lab_host="E. coli XLOLR"
                     /note="Vector: Lambda ZapII; mass excised in plasmid
                     vector pBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
                     mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
                     inoculation  with leaf rust pathogen Puccinia triticina
                     race BBB carrying the  avirulence gene Avr1."
BASE COUNT      100 a    167 c    160 g     91 t
ORIGIN
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  Query Match             12.8%;  Score 204.6;  DB 10;  Length 518;
  Best Local Similarity   79.3%;  Pred. No. 1.1e-29;
  Matches  256;  Conservative    0;  Mismatches   64;  Indels    3;  Gaps    1;

Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
          || ||| ||  |||||||||||||||||| |||||||||||  | ||||||||||| ||||
Db    186 CCAGCGAGGACGCTGCCGGAGACGCCGTCCTGGGCGGTGGCCCTCGTCTTCGCCGTCATG 245

Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
            | ||||||||||||| |||| ||||  ||||| |||||||||||||||||||  |
Db    246 ATCATCGTGTCCGTCCTCCTGGAGCACGCGCTCCATAAGCTCGGCCATTGGTTCCACAAG 305

Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
          |||||||||| || |||  ||||||||||||||||||| ||||||||||||||||||||
Db    306 CGGCACAAGAACGCGCTGGCGGAGGCGCTGGAGAAGATCAAGGCGGAGCTCATGCTGGTG 365

Qy    202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261
          |||||||| || ||||| |||  ||| ||||||||||   |||| ||  ||||||||||
Db    366 GGCTTCATCTCGCTGCTGCTCGCCGTGACGCAGGACCC---CATCTCCGGGATATGCATC 422

Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
          |||||| | ||||||  | ||||| ||||||||||||    | | |    |  |||| |
Db    423 TCCGAGAAGGCCGCCAGCATCATGCGGCCCTGCAAGCTGCCCCCTGGCTCCGTCAAGAGC 482

Qy    322 agcaagtacgttgactactgccc 344
          |   |  | |  |||||||| |
Db    483 AAGTACAAAGACTACTACTGCGC 505
```

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RESULT  12
AV835211
LOCUS       AV835211                408 bp    mRNA    linear   EST 22-JUN-2001
DEFINITION  AV835211 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
            spontaneum top three leaves adult, heading stage Hordeum vulgare
            subsp. spontaneum cDNA clone bah27g01, mRNA sequence.
ACCESSION   AV835211
VERSION     AV835211.1  GI:14527300
KEYWORDS    EST.
SOURCE      Hordeum vulgare subsp. spontaneum.
  ORGANISM  Hordeum vulgare subsp. spontaneum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Hordeum.
REFERENCE   1  (bases 1 to 408)
  AUTHORS   Sato,K.
  TITLE     Barley EST sequencing project in NIG and Okayama Univ
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Kazuhiro Sato
            Research Institute for Bioresources
            Okayama University, Barley Germplasm Center
            Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
            Email: kazsato@rib.okayama-u.ac.jp,
            URL:http://www.rib.okayama-u.ac.jp/barley/
            Sato,K., Saisho,D., Takeda,K., Shini,T. and Kohara,Y. Direct
            submission;
            database:http://www.shigen.nig.ac.jp/barley/Barley.html.
FEATURES             Location/Qualifiers
```

```
    source          1. .408
                    /organism="Hordeum vulgare subsp. spontaneum"
                    /cultivar="H602"
                    /db_xref="taxon:77009"
                    /clone="bah27g01"
                    /clone_lib="K. Sato unpublished cDNA library: Hordeum
                    vulgare subsp. spontaneum top three leaves adult, heading
                    stage"
                    /tissue_type="top three leaves"
                    /dev_stage="adult, heading stage"
BASE COUNT       59 a    120 c    146 g     82 t      1 others
ORIGIN


  Query Match             12.7%;  Score 203.4;  DB 9;  Length 408;
  Best Local Similarity   99.0%;  Pred. No. 1.9e-29;
  Matches  204;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy      1 atgtcggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtg 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    203 ATGTCGGACAAAAAAGGGGTGCCGGCGCGGGAGCTGCCGGAGACGCCGTCGTGGGCGGTG 262

Qy     61 gcggtggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaag 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    263 GCGGTGGTCTTCGCCGCCATGGTGCTCGTGTCCGTCCTCATGGAGCACGGCCTCCACAAG 322

Qy    121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
          ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    323 CTCGGNCATTGGTTCCAGCACCGGCACAAGAAGGCCCTGTGGGAGGCGCTGGAGAAGATG 382

Qy    181 aaggcggagctcatgctggtgggctt 206
          ||||||||||||||||||||||||||
Db    383 AAGGCGGAGCTCATGCTGGTGGGCTT 408


RESULT  13
BG642916
LOCUS       BG642916                620 bp    mRNA    linear   EST 24-APR-2001
DEFINITION  EST511110 tomato shoot/meristem Lycopersicon esculentum cDNA clone
            cTOF26E11 5' sequence, mRNA sequence.
ACCESSION   BG642916
VERSION     BG642916.1  GI:13777942
KEYWORDS    EST.
SOURCE      tomato.
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE   1  (bases 1 to 620)
  AUTHORS   van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Utterback,T.,
            Hansen,C., Ronning,C. and Tanksley,S.
  TITLE     Generation of ESTs from tomato shoot/meristem tissue
  JOURNAL   Unpublished (2001)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html.
FEATURES             Location/Qualifiers
     source          1. .620
                     /organism="Lycopersicon esculentum"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="cTOF26E11"
                     /clone_lib="tomato shoot/meristem"
                     /tissue_type="shoot/meristem"
                     /dev_stage="developing shoots from 4-6wks old plants"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2:
                     Xho1; Small expanding leaves from the growing tip were
                     taken from greenhouse plants (4-6wks old TA496). Tissue
                     was immediately frozen in liquid nitrogen."
BASE COUNT      154 a    123 c    132 g    211 t
ORIGIN


  Query Match             12.0%;  Score 192.6;  DB 10;  Length 620;
  Best Local Similarity   58.2%;  Pred. No. 2.4e-27;
  Matches  358;  Conservative    0;  Mismatches  254;  Indels    3;  Gaps    1;

Qy    354 ggtggcgctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgc 413
          |||  | ||||| || |  | |    |||| ||| | ||| || | |||||| |  | ||
Db      1 GGTCTCTCTCATTTCTATCGACGCACTGCATCAGATACACATCCTTATCTTCTTTTTGGC 60

Qy    414 ggtcttccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaac 473
          |||| | ||||| |  ||||| |  ||||| ||    ||  |    || || ||  |
Db     61 GGTCCTTCATGTGATATACAGTGCTATCACTATGTGGCTGGGAAAACTTAAGATTCGTGG 120

Qy    474 atggaagaaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgc 533
           |||||    |||||   |||||||  |  ||   || ||  ||||  ||||||||||| |
Db    121 CTGGAAATGCTGGGAACAAGAGACCGCAACCCATGACTATGAGTTTTCAAATGATCCTTC 180

Qy    534 acggttccggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctct---ccag 590
          | | ||  || | || ||  |||| || || || |     ||     |  |||   |||
Db    181 AAGATTTAGGCTTACTCATGAGACATCATTTGTCAGAGCACATACTAGTTTCTGGACCAA 240

Qy    591 cacccctggcatcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaa 650
          |  ||   | ||    |   | |      |||||||| || || |||||||| || |  ||
Db    241 TATTCCAATCTTCTTTTACATTGGATGTTTCTTCAGACAATTTTTCAGGTCCGTGAATAA 300

Qy    651 ggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaa 710
          |  || ||| ||||| |  |    ||||| |||| | ||||| | |     || ||
Db    301 GTCAGATTACTTGACCCTCCGCAATGGCTTTATCAGTGTTCATTTAGCTCCTGGAAGTAA 360

Qy    711 gttcgacttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcgg 770
          ||  ||||||| ||||| ||||| |||||  | ||||| ||||||||||| || || ||
Db    361 ATTTAACTTCCAAAAGTATATCAAAAGGTCATTAGAGGATGACTTCAAGGTAGTTGTTGG 420

Qy    771 catcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggt 830
          ||||  |      |||||||        |  |   | |  ||||  |  | | ||||
Db    421 TGTCAGTCCAGTTTTGTGGGGATCATTTGTTGTTTTCTTGCTCCTAAATGTTAGTGGGTG 480

Qy    831 tggcacgctcatctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaa 890
          |  |  | |||  ||| || || ||| |  | ||| | ||   |||||||||  |
Db    481 GCATGCATTGTTTTGGGCTTCCTTAATTCCTTTGATTATCATATTAGCTGTTGGAACACA 540

Qy    891 gctggagatgatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaa 950
          |||  ||  | |  | |     ||||| || || |||  |||  |     ||  || |
Db    541 GCTTCAGGCGGTGTTGACAAGAATGGCTCTTGACATCTCGGAGAGACATGCAGTAGTCCA 600

Qy    951 ggggggcccccgtggt 965
          |||   |||  | ||
Db    601 GGGAATCCCTCTTGT 615


RESULT  14
BI432930
LOCUS       BI432930                643 bp    mRNA    linear   EST 21-AUG-2001
DEFINITION  EST535691 P. infestans-challenged leaf Solanum tuberosum cDNA clone
            PPCAY62 5' sequence, mRNA sequence.
ACCESSION   BI432930
VERSION     BI432930.1  GI:15257620
KEYWORDS    EST.
SOURCE      potato.
  ORGANISM  Solanum tuberosum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
REFERENCE   1  (bases 1 to 643)
  AUTHORS   Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A.,
            Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B.
  TITLE     Generation of ESTs from Potato Leaves Challenged with Phytophthora
            infestans, Compatible Interaction
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Cathy Ronning
```

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          The Institute for Genomic Research
          For clone info: please contact Research Genetics, Libraries
          Division tel 1-800-711-6195, email cdna@resgen.com
          Seq primer: M13F-R.
FEATURES             Location/Qualifiers
     source          1. .643
                     /organism="Solanum tuberosum"
                     /cultivar="Kennebec"
                     /db_xref="taxon:4113"
                     /clone="PPCAY62"
                     /clone_lib="P. infestans-challenged leaf"
                     /tissue_type="leaf"
                     /dev_stage="6 week old"
                     /lab_host="SOLR"
                     /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
                     XhoI; Whole plants were challenged with 450,000
                     sporangia/ml P. infestans US-1(US 940501) in Biotron
                     (Madison, Wisconsin). Leaf tissue was collected at 1, 2,
                     5, 12, and 24 hours post-challenge and frozen in liquid
                     nitrogen immediately upon removal. Kennebec plants showed
                     no signs of HR. Katahdin plants (susceptible to P.
                     infestans US-1) were used as controls and showed
                     infection. NOTE: We cannot exclude the possibility that
                     this sequence is actually derived from Phytophthora rather
                     than potato."
BASE COUNT      154 a    126 c    142 g    221 t
ORIGIN


  Query Match             11.9%;  Score 191;  DB 10;  Length 643;
  Best Local Similarity   57.3%;  Pred. No. 5e-27;
  Matches  364;  Conservative    0;  Mismatches  270;  Indels    1;  Gaps    1;

Qy    587 ccagcacccctggcatcagatgggtggtggccttcttcaggcagttcttcaggtcagtca 646
          | || | |||   | ||   |   | |    ||||||||| || || |||| ||| ||||
Db     10 CAAGGATCCCGATCTTCTTTTACATTGGATGCTTCTTCAGACAATTTTTCAAGTCTGTCA 69

Qy    647 ccaaggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaaca 706
            |||   |||||| || |  || |    || ||||| |  |  ||| || | |     |
Db     70 GTAAGTCAGACTACTTGGCTCTGCGCAATGGTTTCATAAGTGTTCATCTGGCTCCTGGAA 129

Qy    707 gcaagttcgacttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcg 766
          | || || |||||||| ||||| ||||||||||  | ||||| |||||||||| || |
Db    130 GTAAATTTGACTTCCAAAAGTATATCAAGAGGTCATTAGAGGATGACTTCAAGGTAGTTG 189

Qy    767 tcggcatcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatg 826
          ||||  |||| |      | |||||        | ||   | |  | ||  |  | |  |
Db    190 TCGGTGTCAGTCCAGTTTTATGGGGATCATTTGTGCTTTTCTTGCTTCTGAATGTTAGCG 249

Qy    827 gggttggcacgctcatctggatttctttcatccctctcgtgatcctcttgtgtgttggaa 886
          ||       |  |||||   || ||  | |||||  | ||| | ||   ||||||||
Db    250 GGTGGCAAGCATTGTTCTGGGCATCCTTAGTTCCTCTGATTATCATTTTAGCTGTTGGAA 309

Qy    887 ccaagctggagatgatcatcatggagatggccctggagatccaggaccgggcgagcgtca 946
          | |||||  |     |  | |    |||||||||| || ||| | ||  |       ||
Db    310 CAAAGCTTCAAGCTGTTTTGACTAGGATGGCCCTTGACATCAAAGAGAGACATGCAGTAG 369

Qy    947 tcaagggggccccctggtcgagcccagcaacaagttcttctggttccaccgccccgact 1006
          |  | ||   |||  | ||  |  ||    |||| |  || |||||    || ||
Db    370 TTCAAGGAATCCCTCTTGTACAAGCCTCAGACAAATATTTTTGGTTTGGTCGACCACGAC 429

Qy   1007 gggtcctcttcttcatacacctgacgttgttccagaacgcgtttcagatggcgcattttg 1066
           ||| ||   | |||| ||  |  | ||||| ||||| ||||| |||||  |  |||||
Db    430 TGGTTCTTCACCTCATCCATTTTGCCTTGTTTCAGAATGCGTTCCAGATAACATATTTTC 489

Qy   1067 tgtggacagtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagca 1126
          ||||||  |  |      |   || | ||    |    ||||       | |  |||  ||
Db    490 TGTGGATATGGTATGAGTATGGGCTAAAATCTTTGCTCCACGAAGGCGTTGAACTGGTCA 549

Qy   1127 tcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgaccttccccc 1186
          |    ||  | ||  | ||| | |    ||   ||||| ||||| ||||| ||  | || |
Db    550 TTGCAAAAAT-GTTATAGGGGTGGGAGTCTTATTCCTATGCAGTTATATCACTCTTCCAC 608

Qy   1187 tctacgcgctcgtcacacagatgggatcaaacatg 1221
          | || || ||  | || ||||||||||  | |||
Db    609 TTTATGCCCTTATAACTCAGATGGGATCCCATATG 643


RESULT  15
AW934153
LOCUS       AW934153                599 bp    mRNA    linear   EST 18-MAY-2001
DEFINITION  EST359996 tomato fruit mature green, TAMU Lycopersicon esculentum
            cDNA clone cLEF58C7 5', mRNA sequence.
ACCESSION   AW934153
VERSION     AW934153.1  GI:8109554
KEYWORDS    EST.
SOURCE      tomato.
  ORGANISM  Lycopersicon esculentum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids I; Solanales; Solanaceae; Solanum;
            Lycopersicon.
REFERENCE   1  (bases 1 to 599)
  AUTHORS   Alcala,J., Vrebalov,J., White,R., Matern,A.L., Holt,I.E., Liang,F.,
            Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S., Ronning,C.M.
            , Fraser,C.M., Martin,G.B., Tanksley,S.D. and Giovannoni,J.
  TITLE     Generation of ESTs from tomato fruit tissue
  JOURNAL   Unpublished (1999)
COMMENT     Contact: CUGI
            Clemson University Genomics Institute
            Clemson University
            100 Jordan Hall, Clemson, SC 29634, USA
            Email: http://www.genome.clemson.edu/orders/index.html
            5 prime sequence.
FEATURES             Location/Qualifiers
     source          1. .599
                     /organism="Lycopersicon esculentum"
                     /cultivar="TA496"
                     /db_xref="taxon:4081"
                     /clone="cLEF58C7"
                     /clone_lib="tomato fruit mature green, TAMU"
                     /tissue_type="fruit pericarp"
                     /dev_stage="mature green (3-5 days pre-ripening)"
                     /lab_host="SOLR"
                     /note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
                     Xho1; cLEF - Fruit were tagged at the 1cm stage and
                     harvested 3-5 days prior to  ripening. Fruit were cut in
                     half to verify the seeds were indeed  'immature' and the
                     seeds and locules were discarded prior to freezing the
                     pericarp"
BASE COUNT      144 a    116 c    127 g    212 t
ORIGIN


  Query Match             11.9%;  Score 190.2;  DB 9;  Length 599;
  Best Local Similarity   58.0%;  Pred. No. 7e-27;
  Matches  336;  Conservative    0;  Mismatches  243;  Indels    0;  Gaps    0;

Qy    618 cttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcagg 677
          ||||||||| || || |||| ||| ||||  |||   |||||| || |  || |   ||
Db     19 CTTCTTCAGACAATTTTTCAAGTCTGTCAGTAAGTCAGACTACTTGGCTCTGCGCAATGG 78

Qy    678 cttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagag 737
          |||||  |  |  ||| || | |     || || ||  ||||||| ||||||||||||||
Db     79 TTTCATAAGTGTTCATCTGGCTCCTGGAAGTAAATTTAACTTCCAAAAGTACATCAAGAG 138

Qy    738 gtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggc 797
          |||  | ||||| |||||||||||| || |||||  |||| |      | ||||
Db    139 GTCATTAGAGGATGACTTCAAGGTAGTTGTCGGTGTCAGTCCAGTTTTATGGGCATCATT 198

Qy    798 gatcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcat 857
            | ||   | |  | ||  |  | |  |||       |  |  |||||   || || ||
Db    199 TGTGCTTTTCTTGCTTCTGAATGTTAGCGGGTGGCAAGCATTGTTCTGGGCATCCTTAAT 258

Qy    858 ccctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggc 917
          |||||  | ||| | ||   |||||||||| |||||  |     |  | |    ||||||
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Db     259 TCCTCTAATTATCATTTTAGCTGTTGGAACAAAGCTTCAAGCTGTTTTGACTAGGATGGC 318

Qy     918 cctggagatccaggaccgggcgagcgtcatcaagggggcccccgtggtcgagcccagcaa 977
           ||| || ||  | ||  |       ||  |  | ||   |||  | ||  |  ||    |
Db     319 CCTTGACATTAAAGAGAGACATGCAGTAGTTCAAGGAATCCCTCTTGTACAAGCCTCAGA 378

Qy     978 caagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgtt 1037
           ||| |  || |||||    || ||      ||| ||   | |||| ||  |  | |||||
Db     379 CAAATATTTTTGGTTTGGTCGACCACGACTGGTTCTTCACCTCATTCATTTTGCCTTGTT 438

Qy    1038 ccagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaa 1097
           ||||| || || |||||  |  ||||| |||||| |  |     |  ||  | ||
Db     439 TCAGAATGCATTCCAGATAACATATTTTCTGTGGATATGGTATGAGTATGGGCTAAAATC 498

Qy    1098 atgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctcca 1157
           |||| ||||  |  | | | ||||  |||   ||  | ||  | ||  | |   ||
Db     499 TTGCTTCCACGAGGCGTTTGAGCTGGTCATTGCAAAAATTGTTATAGGAGTGGGAGTCTT 558

Qy    1158 gttcctctgcagctatatgaccttccccctctacgcgct 1196
           ||||| ||||| ||||| ||  | || || || || ||
Db     559 ATTCCTATGCAGTTATATCACTCTTCCGCTTTATGCCCT 597
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Search completed: July 23, 2002, 10:04:44
Job time: 3857 sec

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 09:37:07 ; Search time 54.2 Seconds
(without alignments)
7260.238 Million cell updates/sec

Title: US-09-722-377-2
Perfect score: 1602
Sequence: 1 atgtcggacaaaaaaggggt.....tttccttcagccagggatga 1602

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	425.2	26.5	1851	4	US-09-183-959-9	Sequence 9, Appli
2	312	19.5	1040	4	US-09-183-959-11	Sequence 11, Appl
3	294.6	18.4	538	4	US-09-183-959-13	Sequence 13, Appl
4	225.4	14.1	1869	4	US-09-350-268-1	Sequence 1, Appli
5	216.6	13.5	1725	4	US-09-183-959-1	Sequence 1, Appli
6	148.8	9.3	1831	4	US-09-183-959-7	Sequence 7, Appli
7	117.2	7.3	705	4	US-09-183-959-17	Sequence 17, Appl
8	83.6	5.2	597	4	US-09-183-959-3	Sequence 3, Appli
9	80.4	5.0	750	4	US-09-183-959-18	Sequence 18, Appl
10	59	3.7	472	4	US-09-183-959-5	Sequence 5, Appli
11	51.2	3.2	1575	1	US-07-988-260B-2	Sequence 2, Appli
12	49.4	3.1	1392	3	US-08-478-097A-37	Sequence 37, Appl
C 13	47.6	3.0	4451	3	US-08-717-294-42	Sequence 42, Appl
14	47.4	3.0	1004	1	US-07-841-646-10	Sequence 10, Appl
15	47.4	3.0	1004	1	US-08-147-023-10	Sequence 10, Appl
16	47.4	3.0	1004	1	US-08-447-570-10	Sequence 10, Appl
17	47.4	3.0	1004	2	US-08-449-700-10	Sequence 10, Appl
18	47.4	3.0	1004	2	US-08-449-699A-10	Sequence 10, Appl
19	47.4	3.0	1259	1	US-07-764-731B-9	Sequence 9, Appli
20	47.4	3.0	1277	1	US-07-841-646-14	Sequence 14, Appl
21	47.4	3.0	1277	1	US-08-147-023-14	Sequence 14, Appl
22	47.4	3.0	1277	1	US-08-447-570-14	Sequence 14, Appl
23	47.4	3.0	1277	2	US-08-449-700-14	Sequence 14, Appl
24	47.4	3.0	1277	2	US-08-449-699A-14	Sequence 14, Appl
25	47.4	3.0	1295	1	US-08-256-368-1	Sequence 1, Appli
26	47.4	3.0	1448	1	US-07-539-756-3	Sequence 3, Appli
27	47.4	3.0	1448	1	US-08-377-292-7	Sequence 7, Appli
28	47.4	3.0	1448	2	US-07-989-847-5	Sequence 5, Appli
29	47.4	3.0	1448	4	US-08-469-411-5	Sequence 5, Appli
30	47.4	3.0	1505	1	US-07-841-646-12	Sequence 12, Appl
31	47.4	3.0	1505	1	US-08-147-023-12	Sequence 12, Appl
32	47.4	3.0	1505	1	US-08-447-570-12	Sequence 12, Appl
33	47.4	3.0	1505	2	US-08-449-700-12	Sequence 12, Appl
34	47.4	3.0	1505	2	US-08-449-699A-12	Sequence 12, Appl
35	47.4	3.0	1822	1	US-07-841-646-1	Sequence 1, Appli
36	47.4	3.0	1822	1	US-07-901-703-1	Sequence 1, Appli
37	47.4	3.0	1822	1	US-08-147-023-1	Sequence 1, Appli
38	47.4	3.0	1822	1	US-08-206-864-1	Sequence 1, Appli
39	47.4	3.0	1822	1	US-08-278-729A-16	Sequence 16, Appl
40	47.4	3.0	1822	1	US-08-480-528A-3	Sequence 3, Appli
41	47.4	3.0	1822	1	US-08-479-666-3	Sequence 3, Appli
42	47.4	3.0	1822	1	US-08-155-343A-16	Sequence 16, Appl
43	47.4	3.0	1822	1	US-08-406-672-16	Sequence 16, Appl
44	47.4	3.0	1822	1	US-08-643-563A-16	Sequence 16, Appl
45	47.4	3.0	1822	1	US-08-447-570-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-183-959-9
; Sequence 9, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 9
; LENGTH: 1851
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-9

Query Match 26.5%; Score 425.2; DB 4; Length 1851;
Best Local Similarity 66.0%; Pred. No. 3.4e-85;
Matches 632; Conservative 0; Mismatches 323; Indels 3; Gaps 1;

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Qy    336 ctactgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgt 395
          | | ||||| ||||| || ||| ||||||| ||||    |  | ||||||||||||||| |
Db    587 caagtgccccgaggggaaagtgccgctcatctccatcaacgccctgcaccagctgcacat 646

Qy    396 cttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaag 455
          |||||||||| | ||||| |||||||| ||| |||||||||  |||||||| || ||  |
Db    647 cttcatcttcttcctcgccgtcttccacgtctcctacagcgcaatcaccatggcgctcgg 706

Qy    456 ccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctccttggaatacca 515
          | |   ||| ||  |  |||||||  | ||||||| |||  |  |       || ||| |
Db    707 cagggccaagatacgtgcatggaaagagtgggagaaagaagctgcaggacaagactacga 766

Qy    516 gttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcgcca 575
          |||| || |||| ||  | |||||| ||||||| ||| |||| || ||||||| ||  ||
Db    767 gttctcacatgacccgacgcggttcaggttcacccacgagacttccttcgtgaggcagca 826

Qy    576 cctg---ggcctctccagcacccctggcatcagatgggtggtggccttcttcaggcagtt 632
            ||   |  ||   ||    ||| |         |   |      ||||||| |||||||
Db    827 tatgaatgtgctgaacaagttcccagcatcattctacatcagcaacttcttccggcagtt 886

Qy    633 cttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgca 692
          ||||||||| || |   |||  ||||||    |  || |     ||||  ||||||  ||
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Db    887 cttcaggtccgtgaggcaggcagactactgcgcgctgcgccacagctttgtcaacgtcca 946

Qy    693 tttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcgatggaggacga 752

Db    947 tctggcccctggcagcaagtttgatttccagaagtacatcaagcggtctctggaggatga 1006

Qy    753 cttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctctt 812

Db   1007 cttcaaggtgatcgtggggatcagtcctcctctgtgggcttctgctctcatcttcctctt 1066

Qy    813 ccttgacatcaatggggttggcacgctcatctggatttctttcatccctctcgtgatcct 872

Db   1067 cctcaacgtcaatggatggcacaccatgctctggatctccatcatgccggtggtgatcat 1126

Qy    873 cttgtgtgttggaaccaagctggagatgatcatcatggagatggccctggagatccagga 932

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Qy    933 ccgggcgagcgtcatcaagggggccccccgtggtcgagcccagcaacaagttcttctggtt 992

Db   1187 gcgccacgccgtcatccagggcatcccgatggtgcaagtcagcgactcctacttctggtt 1246

Qy    993 ccaccgccccgactgggtcctcttcttcatacacctgacgttgttccagaacgcgtttca 1052

Db   1247 cgcacgccccaccttcgtgctcttcctcatccacttcaccctcttccagaatggcttcca 1306

Qy   1053 gatggcgcattttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgca 1112

Db   1307 gatcatctacttcctctggattctgtatgagtacggcatggactcgtgcttcaacgactc 1366

Qy   1113 gatcgggctgagcatcatgaaggtggtggtggggctagctctccagttcctctgcagcta 1172

Db   1367 cgaagagttcgtctttgcacgactctgccttggcgtggttgtccaggtgctgtgcagcta 1426

Qy   1173 tatgaccttccccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccat 1232

Db   1427 cgtgacgctcccgctgtacgcgctcgtctcccaaatgggctccaccatgaagcagtccat 1486

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Db   1487 cttcgacgagcagacctccaaggcgctcaagaactggcgcgccggcgccaagaagaag 1544


RESULT   2
US-09-183-959-11
; Sequence 11, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 11
;   LENGTH: 1040
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-183-959-11


  Query Match             19.5%;  Score 312;  DB 4;  Length 1040;
  Best Local Similarity   64.4%;  Pred. No. 2.8e-60;
  Matches  484;  Conservative    0;  Mismatches  265;  Indels    3;  Gaps    1;

Qy    542 ggttcacgcaccagacgtcgttcgtgaagcgccacctg---ggcctctccagcacccctg 598

Db      2 ggttcacccacgagacttcgtttgtgaggcagcatatgaatgtgctcaacaagttcccag 61

Qy    599 gcatcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggact 658

Db     62 catccttctacatcagcaacttcttccggcagttcttcaggtccgtcaggcgggcagact 121

Qy    659 acctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgact 718

Db    122 actgcgcgctgcgccacagctttgtcaacgtccatctggcccctggcaccaagtttgatt 181

Qy    719 tccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcc 778

Db    182 tccaaaagtacatcaagcggtctctggaggacgacttcaaggtgatcgtggggatcagcc 241

Qy    779 tcccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgc 838

Db    242 ctcctttgtgggcttctgctctcatcttcctattcctcaatgtcaatggatggcacacca 301

Qy    839 tcatctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggaga 898

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Qy    899 tgatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggccc 958

Db    362 gcatcatctgccgcatggcgatcgacatcacggagcggcacgccgtgatccagggcatcc 421

Qy    959 ccgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttct 1018

Db    422 cgctggtgcaggtcagcgactcctacttctggttcgcacgcccaaccttcgtgctcttcc 481

Qy   1019 tcatacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtgg 1078

Db    482 tcatccacttcaccctcttccagaatggcttccagatcatctacttcctctggattctgt 541

Qy   1079 ccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtgg 1138

Db    542 atgagtacgggatggactcgtgcttcaacgactccgaagaattcgtctttgcacgtctct 601

Qy   1139 tggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcg 1198

Db    602 gccttggggtggttgttcaggtgctgtgcagctacgtgacgctccctctgtacgcgctcg 661

Qy   1199 tcacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgc 1258

Db    662 tctcccagatgggctccaccatgaagcagtccatcttcgacgagcagacctccaaggcgc 721

Qy   1259 tcaccaactggcggaacacggccaaggagaag 1290

Db    722 tcaagaactggcgcgccggcgccaagaagaag 753


RESULT   3
US-09-183-959-13
; Sequence 13, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 13
;   LENGTH: 538
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
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;   NAME/KEY: unsure
;   LOCATION: (479)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (492)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (499)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (518)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (530)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (537)
US-09-183-959-13
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Query Match 18.4%; Score 294.6; DB 4; Length 538;
Best Local Similarity 76.0%; Pred. No. 1.7e-56;
Matches 376; Conservative 0; Mismatches 116; Indels 3; Gaps 1;

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Db      1 gtggagccaagtgacaggttcttctggtttaaccgccctggctgggtcctcttcctcatc 60

Qy   1024 cacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccacg 1083
          ||||| ||| | |||||||||||| || |||||||||||||| || |||||| ||  |||
Db     61 cacctcacgctcttccagaacgccttccagatggcgcatttcgtttggacactgctcacc 120

Qy   1084 cccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggtg 1143
          || | | ||||||||||||||||||  |  | | || ||||||||||||||| || | ||||
Db    121 ccagacctgaagaaatgctaccacgagaggctgggcctgagcatcatgaaagttgcggtg 180

Qy   1144 gggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcaca 1203
          ||||| | ||||||| |||||||||||||| || |||||||| ||||||||||||||||||
Db    181 gggctggttctccaggtcctctgcagctacatcaccttcccgctctacgcgctcgtcacg 240

Qy   1204 cagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcacc 1263
          |||||||| ||  ||||||||| | |||||||||| |||||||| ||||||| | |
Db    241 cagatggggtcgcacatgaagaagaccatcttcgaggagcagacggccaaggcggtgatg 300

Qy   1264 aactggcggaacacggccaaggagaagaagaaagtccgagacacg---gacatgctgatg 1320
          || ||||| || |||||||||| ||| |       || ||  ||   | | | ||
Db    301 aagtggcgcaagacggccaaggataaggtgcggcagcgggaggcggcaggcttcctcgac 360

Qy   1321 gctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggc 1380
          |  | || || || |||| | || |||||||   ||    || ||  ||||||||||||||
Db    361 gtgctgacgagcgccgacaccacgccgagccacagccgcgcgacgtcgccgagccggggc 420

Qy   1381 tcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcg 1440
             || || |||||||||| ||||||  || |||  ||||||| || || ||||| | |
Db    421 aactcgccggtgcacctgctccacaagtacaggggcaggtcggaggaaccgcagagggng 480

Qy   1441 cccacctcgccaagg 1455
          ||  | ||||  ||
Db    481 ccggcgtcgcgnggg 495
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RESULT 4
US-09-350-268-1
; Sequence 1, Application US/09350268
; Patent No. 6211433
; GENERAL INFORMATION:
;  APPLICANT: Simmons, Carl R.
;  TITLE OF INVENTION: Methods and Compositions to Enhance Disease Resistance
;  TITLE OF INVENTION: in Plants
;  FILE REFERENCE: 5718-42A-- Mlo3
;  CURRENT APPLICATION NUMBER: US/09/350,268
;  CURRENT FILING DATE: 1999-07-06
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1869
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   OTHER INFORMATION: Mlo3
US-09-350-268-1
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Query Match 14.1%; Score 225.4; DB 4; Length 1869;
Best Local Similarity 52.5%; Pred. No. 4.2e-41;
Matches 702; Conservative 0; Mismatches 546; Indels 89; Gaps 6;

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Db     92 ggaggcgacgctggaggacacgcctacgtggatcgtggcgtccgtgtgctccgtcatcgt 151

Qy     84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
           ||| | ||| || || | || | ||  |||||| | |||||| |     |  ||| |||
Db    152 cctcatctccttcgtcttcgagcgcgcgctccaccacctcggcaaggcactggagcgccg 211

Qy    144 gcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtggg 203
          |   | |||| ||||||  |||||||||    ||| | || |  ||||||||||||| ||||
Db    212 g---aggaagaccctgtacgaggcgctgctaaagctcaaagaagagctcatgctgctggg 268

Qy    204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
          |||| | || |||||||||| ||||| | |||||   | | ||    ||||| ||||||
Db    269 cttcgtctcgctgctcctcgtcgtctcccagga---cttgatacagaagatctgcatcga 325

Qy    264 cgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccag 323
          |||     |   ||   |  |  ||| ||| | | |  | ||    |  |  | |
Db    326 cgacagcctcatggagcactggatgccgtgccggggtgcgagcgccaccgcctcggctca 385

Qy    324 caagtacgttgactactgcccgg---------------------------------- 346
            |    ||   || || | |
Db    386 ttacggtgtctcctcctcctcctcctcctccgcggtcggtggcgggaggaggatgctcaa 445

Qy    347 ----------------------------------agggcaaggtggcgctcatgtccac 371
                                             |||| || ||  || |  | ||
Db    446 aggcggcggggcagctttcgggcactgttcaagcaagggaaaagtcccgttgctatcact 505

Qy    372 gggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcaccta 431
            |  |||| | ||| | ||| | |||||||||||| || ||  ||   || |||
Db    506 tcacgccttggagcaggtacacattttcatcttcgtcctagctatcacgcaagtcgttct 565

Qy    432 cagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggag-a 490
          |||||||  |||| |    ||  | | |||  | ||| | | ||||| | | |||||| |
Db    566 cagcgtcgccaccgtcctcctgggacttctgcagatgcggatatggatgcactgggagaa 625

Qy    491 cagagaccacctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgc 550
          ||     || |     || |   | | || |||       |  |   || | |     |
Db    626 caccattcagcaagagggcagctctgctcccaagatgatcgcccgtgtgcagaaaatcag 685

Qy    551 accagacgtcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatggg 610
                |   | ||    | |  |   |  |         | ||    |  || | ||||
Db    686 gttcatccaggaccg----gtgtaaggggtacgagaaggccgcctgggttataatatggc 741

Qy    611 tggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttga 670
          ||    | |||||||  |||||||  | | |||||  |||| |  |||||| |  |  |||
Db    742 tgcgttctttcttcaaacagttctacggatcagtgtccaacgacgactacattgcgatga 801

Qy    671 gggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtaca 730
          |    || ||| |||  | ||| ||    |     ||  |||||||  ||||  || | ||||
Db    802 gactcggtttcgtcatggagcactttaggggcaccccaagttcaacttttacgactaca 861

Qy    731 tcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggg 790
          | | |   |  | ||| | || ||||||   || ||  | || |              |||
Db    862 tgatcaaagctctcgagaaagatttcaagcgagtagttagtataaaatggtattactgga 921

Qy    791 gtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctcatctggattt 850
          | | | |||  ||   ||  | ||  |  |||  |||     | |   | |||||||  |
Db    922 ttttgtgatgatctttctgctgctcaatgtcaccgggtggcactcctacttctggatct 981
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Qy    851 ctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatgg 910
Db    982 cattagttccactggctctgctgcttctgattgggacgaagctggagcacatcataaaca 1041

Qy    911 agatggccctggagat------ccaggaccgggcgagcgtcatcaaggggcccccgtgg 964
Db   1042 ggctggcctacgaggtggcctcgaagcacgccgccgggcaaggcgaaggggcatcgtgg 1101

Qy    965 tcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcatac 1024
Db   1102 tgagcccttcggacgagctgttctggttccgcagcccacggctggtgctcgtgctcatcc 1161

Qy   1025 acctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccacgc 1084
Db   1162 acttcatcctgttccagaacgcgttcgagttcgcgtatttcttctggacactggcgatgt 1221

Qy   1085 ccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggtgg 1144
Db   1222 tcggcgccaactcctgcatcatggacagtctaggatacagcgtctcgcgaatcatcatat 1281

Qy   1145 ggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcacac 1204
Db   1282 gcgtcgtcgtccaggtgctctgcagctacagcacactcccgctctacgccatcgtgtccc 1341

Qy   1205 agatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcacca 1264
Db   1342 atatggggagttcgttcaagagcgctgtgttcgtggacgacgtcgccgacaatctcagag 1401

Qy   1265 actggcggaacacggcc 1281
Db   1402 ggtgggccgacggcgcc 1418
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RESULT 5
US-09-183-959-1
; Sequence 1, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 1
; LENGTH: 1725
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-1

Query Match 13.5%; Score 216.6; DB 4; Length 1725;
Best Local Similarity 51.4%; Pred. No. 3.6e-39;
Matches 692; Conservative 0; Mismatches 574; Indels 81; Gaps 5;

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Qy     24 ggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatggt 83
Db     20 ggcggcggcgctggagttcacaccgacgtggatcgtcgcggcggtctgctctctcatcgt 79

Qy     84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
Db     80 gctcctctcgctcgtcgccgagcgatgcctccactacctcggcaagacgctcaagaggaa 139

Qy    144 gcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtggg 203
Db    140 gaaccagaagccgctcttcgaggcgctgctcaaggtcaaagaagagttgatgcttctggg 199

Qy    204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
Db    200 gttcatctccctgctgctgacggtgttccagg---ggatgatccggaggacgtgcatccc 256

Qy    264 cgaggatgccgccgacgtcatgtggccctgcaa---------------------------- 296
Db    257 tgaacgctggacattccacatgctgccatgcgagaagccagatgagaaggccggtgaggc 316

Qy    297 ----------gcgcggcaccgagggccgcaagcccagcaagtacgttgactactgc---- 342
Db    317 cgccaccatggagcattttgtagggacgcttggcaggatcggtaggcgtctgttgcagga 376

Qy    343 ----------------------------ccggagggcaaggtggcgctcatgtccacggg 374
Db    377 aggcactgctggggctgagcaatgccagaagaagggaaaagttccacttttgtcccttga 436

Qy    375 cagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacag 434
Db    437 agccatacatcagctgcacattttcatatttgttctggcaatcacacatgttattttcag 496

Qy    435 cgtcatcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacaga 494
Db    497 cgtcacaactatgcttttaggaggtgcacagatacaccaatggaaacagtgggagaatgg 556

Qy    495 gaccacctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcacca 554
Db    557 aatta------aaaaagatgctcctggaaatgggcctaaggtaaccaatgtacatcatca 610

Qy    555 gacgtcgttcgtgaagcgccacctgggcctctccagcacccctggca---tcagatgggt 611
Db    611 tgaatttatcaagaaacgttttaagggtattggcaaagattctataatattgagttggct 670

Qy    612 ggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgag 671
Db    671 gcattcttttggtaagcagttttatagatcagtatctaaatcagattacaccacaatgcg 730

Qy    672 ggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacat 731
Db    731 tcttggttttatcatgactcactgccctggaaatccaaaatttgatttccatagatacat 790

Qy    732 caagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtgggg 791
Db    791 ggtaagggttttagaggcggattttaagaaagtggtaggcataagctggtacttgtgggt 850

Qy    792 tgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttc 851
Db    851 cttcgtggtgatatttctgttgctgaatgttaatggctggcacacatacttttggattgc 910

Qy    852 tttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatgga 911
Db    911 tttccttcccctattcttctgttagccattggcactaagctggagcatgtcatagctca 970

Qy    912 gatggccctggagatccaggaccgggcgagcgtcatcaaggggcccccgtggtcgagcc 971
Db    971 gctagcccatgatgtagctgagaagcacacagcggtcgagggcgatgtgatcgtaaaacc 1030

Qy    972 cagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgac 1031
Db   1031 atcagatgaacacttctggttcggcaagcctagggttatcctttacctgatccacttcat 1090

Qy   1032 gttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggctt 1091
Db   1091 cctctttcagaatgcgtttgagattgcgtttttcttctggatactgagcacttatggatt 1150

Qy   1092 gaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagc 1151
Db   1151 cgactcgtgcatcatgggacaagttcgttttattgtgccaaggcttgtcatcggggtggt 1210

Qy   1152 tctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcacacagatggg 1211
Db   1211 tattcagcttctctgcagctacagcaccttgcctctgtatgcaattgtaacccagatggg 1270
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Qy   1212 atcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcg 1271
Db   1271 gagctgctacaagaaggagatcttcaacgagcatgtgcagcagggcgtcctgggctgggc 1330

Qy   1272 gaacacggccaaggagaagaagaaagt 1298
Db   1331 tcagaaggtcaagatgaaaaagggact 1357
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RESULT 6
US-09-183-959-7
; Sequence 7, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Microsoft Windows 95
; SEQ ID NO 7
; LENGTH: 1831
; TYPE: DNA
; ORGANISM: Zea mays
US-09-183-959-7

Query Match 9.3%; Score 148.8; DB 4; Length 1831;
Best Local Similarity 48.0%; Pred. No. 3.4e-24;
Matches 638; Conservative 0; Mismatches 632; Indels 60; Gaps 5;

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Qy     16 ggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgcc 75
Db     79 gcggagcaggggcggtcgctggcggagacgcccacctggtccgtggcaaccgtcaccacg 138

Qy     76 gccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttc 135
Db    139 ctcatggtcgctgcctgcttcctcgtcgagcgctccctctcgcgcttcgccaagtggctg 198

Qy    136 cagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatg 195
Db    199 cgcaagaccaagcggaaggccatgctcgccgcgctcgagaagatccgcgaagagctgatg 258

Qy    196 ctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagata 255
Db    259 ctgctcggagtcatctcgctgctgctcagccagacggcgcgcttcatatcggagatctgc 318

Qy    256 tgcatctccgaggatgccgccgacgtcatgtggccctg---caagcgcggcaccgagggc 312
Db    319 gtgccgtcctcgctcttcaccagccgcttctacatctgctccgagagcgactaccaggac 378

Qy    313 cgcaagcccagcaagtacgttgacta---------------------------------- 338
Db    379 ctgctgcgcaacacggacgccaaccagacggcgctcgacaagaacatgttcggtggccaa 438

Qy    339 ----------ctgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccag 387
Db    439 cggctgcacgtctgtggcgagggccatgaacctttgtttcgtacgagggccttgagcag 498

Qy    388 ctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccata 447
Db    499 ctgcaccggtttctcttcatccttggtatcactcatgtgttgtacagttttgtaacagtg 558

Qy    448 gctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctccttg 507
Db    559 gttctgtccatgatcaagatctatagctggaggaagtgggaaaccttagcaggtccaatt 618
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Qy    508 gaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtg 567
Db    619 gctgctgaggaattgaaagctaggagaaccaaggtgatgagaaggcagtcaacctttgtt 678

Qy    568 aagcgccacctgggcctctccagcacccctggca------tcagatgggtggtggccttc 621
Db    679 tttaacaatgcttctcatccatggagcaaaaataaaatacttatttggatgctttgcttt 738

Qy    622 ttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttc 681
Db    739 ttgcgtcaattcaagggctccataataaggtcagactatttggcactgaggttgggcttt 798

Qy    682 atcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcg 741
Db    799 gtca---catatcacaagctaccacattcatatgacttccataaatacatggtacggagc 855

Qy    742 atggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatc 801
Db    856 atggaagatgattacaatgggactattggtatcagttggccacttgggcatatgcgatt 915

Qy    802 ctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatccct 861
Db    916 gtctgcatattaatcaatgttcatggtatcaatatatatttctggttgtcctttgttcct 975

Qy    862 ctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggccctg 921
Db    976 gttattctggtgcttctagtgggtactgaacttcagcacgtcattgctcagttggctttg 1035

Qy    922 gagatccaggaccgggcgagcgtcatcaaggggccccccgtggtcgagcccagcaacaag 981
Db   1036 gaagtcgctga---ggcaacagcgccttatgttggctcacaacttaaactgcgtgatgat 1092

Qy    982 ttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttccag 1041
Db   1093 ctattttggtttggaaagcctcgggtactctggtggcttatacagttcatttcatttcag 1152

Qy   1042 aacgcgtttcagatggcgcatttttgtgtggacagtggccacgcccggcttgaagaaatgc 1101
Db   1153 aatgcttttgagctggcaacattcttatggtctctgtgggaactcagtgcacaaacatgt 1212

Qy   1102 taccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccagttc 1161
Db   1213 ttcatgaagcactactacatggttgccattcggttgatttctgggctcttagttcagttt 1272

Qy   1162 ctctgcagctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaacatg 1221
Db   1273 tggtgcagctacagcacactcccgctgaatgtgattatttctcagatgggtcccaagttc 1332

Qy   1222 aagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacggcc 1281
Db   1333 aagaaatcactggtctcggagaacgtgagggagtcgctgcacagctggtgcaagagggtt 1392

Qy   1282 aaggagaaga 1291
Db   1393 aaggacagga 1402
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RESULT 7
US-09-183-959-17
; Sequence 17, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Miao, Guo-Hua
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Taramino, Graziana
; TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
; FILE REFERENCE: BB-1125
; CURRENT APPLICATION NUMBER: US/09/183,959
; CURRENT FILING DATE: 1998-11-02
; EARLIER APPLICATION NUMBER: 60/064,493
; EARLIER FILING DATE: No. 6303332ember 5, 1997
; NUMBER OF SEQ ID NOS: 20

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;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 17
;   LENGTH: 705
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-183-959-17


  Query Match             7.3%;  Score 117.2;  DB 4;  Length 705;
  Best Local Similarity   72.4%;  Pred. No. 2.5e-17;
  Matches  152;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy     618 cttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcagg 677
           ||||||| |||||||||||||||| || |   |||  ||||||    |  || |     |
Db     175 cttcttccggcagttcttcaggtccgtgaggcaggcagactactgcgcgctgcgccacag 234

Qy     678 cttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagag 737
           |||  ||||||  ||| || | |    ||||||||| || ||||| ||||||||||| |
Db     235 ctttgtcaacgtccatctggcccctggcagcaagtttgatttccagaagtacatcaagcg 294

Qy     738 gtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggc 797
           |||  ||||||| ||||||||||  |||| || ||||| |  || |||||||  |   ||
Db     295 gtctctggaggatgacttcaaggtgatcgtggggatcagtcctcctctgtgggcttctgc 354

Qy     798 gatcctcacccctcttccttgacatcaatgg 827
             || ||  |||||||||  || |||||||
Db     355 tctcatcttcctcttcctcaacgtcaatgg 384


RESULT   8
US-09-183-959-3
; Sequence 3, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 3
;   LENGTH: 597
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (3)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (475)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (520)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (538)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (540)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (552)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (559)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (568)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (571)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (583)
US-09-183-959-3


  Query Match             5.2%;  Score 83.6;  DB 4;  Length 597;
  Best Local Similarity   54.6%;  Pred. No. 6.3e-10;
  Matches  189;  Conservative    0;  Mismatches  154;  Indels    3;  Gaps    1;

Qy     713 tcgacttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggca 772
           | || |||||||| ||||| |   |  |  | ||  | || || ||    || || || |
Db      34 ttgatttccacaaatacatgactcgcgctgttgaatatgagtttaaaagagttgttggta 93

Qy     773 tcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttg 832
           |||||      ||||||  | | |  ||| |   |||  | ||  | || |||||
Db      94 tcagctggtatctgtggctttttgtaatcttattcctgctgctgaatataaatggatggc 153

Qy     833 gcacgctcatctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagc 892
           |||   | ||||| |  ||||| | |||||  |  |  |  |   ||||||  |||| |
Db     154 acacatacttctggttggctttcttgcctctatttctgttacttattgttggtgccaaac 213

Qy     893 tggagatgatcatcatggagatggccctggagatccag---gaccgggcgagcgtcatca 949
           | |||   || ||||    | |||| |  |||     |          | |     |
Db     214 tagagcacattatcactcggttggctcaagaggcagcgatatcattatcaaataatacag 273

Qy     950 agggggcccccgtggtcgagcccagcaacaagttcttctggttccaccgccccgactggg 1009
           |||  |  ||     | ||||  ||||  |    |||||||| |||   || ||    |
Db     274 aggaagttccgaaaataaagccatgcaaggaccatttctggtttcacaagcctgagctag 333

Qy    1010 tcctcttcttcatacacctgacgttgttccagaacgcgtttcagat 1055
           ||||    || || ||  | |  ||||||||||  ||||  ||||
Db     334 tccttcatttgattcatttcatcctgttccagaattcgttcgagat 379


RESULT   9
US-09-183-959-18
; Sequence 18, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 18
;   LENGTH: 750
;   TYPE: DNA
;   ORGANISM: Zea mays
US-09-183-959-18


  Query Match             5.0%;  Score 80.4;  DB 4;  Length 750;
  Best Local Similarity   71.9%;  Pred. No. 3.4e-09;
  Matches  105;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy     682 atcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcg 741
           ||  | |  ||| || | |    || |||||| || ||||| |||||||||||| ||||
Db     304 atgcaggtccatctggcccctggcaccaagtttgatttccaaaagtacatcaagcggtct 363

Qy     742 atggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatc 801
           ||||||||||||||||||  |||| || |||||||  ||  ||||||  |   ||  ||
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Db    364 ctggaggacgacttcaaggtgatcgtggggatcagccctcctttgtgggcttctgctctc 423

Qy    802 ctcaccctcttccttgacatcaatgg 827
          ||  ||| |||||  |  |||||||
Db    424 atcttcctattcctcaatgtcaatgg 449


RESULT  10
US-09-183-959-5
; Sequence 5, Application US/09183959
; Patent No. 6303332
; GENERAL INFORMATION:
;  APPLICANT: Cahoon, Rebecca E.
;  APPLICANT: Miao, Guo-Hua
;  APPLICANT: Rafalski, J. Antoni
;  APPLICANT: Taramino, Graziana
;  TITLE OF INVENTION: CORN cDNA ENCODING SOUTHERN LEAF BLIGHT RESISTANCE
;  FILE REFERENCE: BB-1125
;  CURRENT APPLICATION NUMBER: US/09/183,959
;  CURRENT FILING DATE: 1998-11-02
;  EARLIER APPLICATION NUMBER: 60/064,493
;  EARLIER FILING DATE: No. 6303332ember 5, 1997
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: Microsoft Windows 95
; SEQ ID NO 5
;   LENGTH: 472
;   TYPE: DNA
;   ORGANISM: Zea mays
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (164)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (351)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (379)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (398)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (414)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (427)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (439)..(440)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (447)
;   FEATURE:
;   NAME/KEY: unsure
;   LOCATION: (450)
US-09-183-959-5


  Query Match             3.7%;  Score 59;  DB 4;  Length 472;
  Best Local Similarity   58.7%;  Pred. No. 0.00016;
  Matches  101;  Conservative    0;  Mismatches   71;  Indels    0;  Gaps    0;

Qy   1145 ggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcacac 1204
          || | | | | ||  | |||||||||||| |  ||||| || || || ||  | || || |
Db    151 gggtggttattcancttctctgcagctacagcaccttgcctctgtatgcaattgtaaccc 210

Qy   1205 agatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcacca 1264
          |||||||      |   |||| |   |||||| |||||||   |    |||   ||
Db    211 agatggggagctgctacaagaaggagatcttcaacgagcatgtgcagcagggcgtcctgg 270

Qy   1265 actggcggaacacggccaaggagaagaagaaagtccgagacacggacatgct 1316
          ||||    | | || ||||  ||| |||  | |  | ||   | |  ||||
Db    271 gctgggctcagaaggtcaagatgaaaaagggactgagggagctgcatctgct 322
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RESULT  11
US-07-988-260B-2
; Sequence 2, Application US/07988260B
; Patent No. 5482843
;  GENERAL INFORMATION:
;    APPLICANT:  BRZEZINSKI, RYSZARD
;    TITLE OF INVENTION:  ENZYME OF USE IN CHITOSAN
;    TITLE OF INVENTION:  HYDROLYSIS
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CUSHMAN, DARBY & CUSHMAN
;      STREET:  1100 New York Avenue, N.W., 9th Floor
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  U.S.A.
;      ZIP:  20005-3918
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch, 720 kb diskette
;      COMPUTER:  IBM PS/2, Model 30
;      OPERATING SYSTEM:  PC-DOS 3.30
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/988,260B
;      FILING DATE:  19921214
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hymo, Lawrence A.
;      REGISTRATION NUMBER:  19,057
;      REFERENCE/DOCKET NUMBER:  LAH/3122/98214/MJW
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 861-3000
;      TELEFAX:  (202) 822-0944
;      TELEX:  6714627 CUSH
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1575 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:  Streptomyces N174
US-07-988-260B-2


  Query Match             3.2%;  Score 51.2;  DB 1;  Length 1575;
  Best Local Similarity   47.8%;  Pred. No. 0.011;
  Matches  149;  Conservative    0;  Mismatches  163;  Indels    0;  Gaps    0;

Qy     75 cgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggtt 134
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Db    635 CACCAAGGACTGGGCGACCGCCGCCAAGGACACCGTCTTCCAGCAGGCCCAGAACGACGA 694

Qy    135 ccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcat 194
            |  |||||  | |    | || |   |     | || ||||    | |    || |
Db    695 GCGCGACCGGGTCTACTTCGACCCGGCCGTCAGCCAGGCGAAGGCCGACGGCCTGCGCGC 754

Qy    195 gctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagat 254
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Db    755 GCTGGGCCAGTTCGCCTACTACGACGCCATCGTGATGCACGGCCCCGGCAACGACCCGAC 814

Qy    255 atgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccg 314
            || ||   |       |     || ||||  |     || |  |  | || ||||| |
Db    815 CAGCTTCGGTGGCATCCGCAAGACCGCCATGAAGAAGGCCAGGACCCCCGCCCAGGGCGG 874

Qy    315 caagcccagcaagtacgttgactactgcccggagggcaaggtggcgctcatgtccacgggg 374
          | |    | ||  ||| | ||  || || ||| | |     |||   |||| ||| |
Db    875 CGACGAGACCACCTACCTCAACGCCTTCCTGGACGCCCGCAAGGCCGCCATGCTCACCGA 934

Qy    375 cagcttgcacca 386
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Db    935 GGCCGCGCACGA 946
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RESULT  12
US-08-478-097A-37
; Sequence 37, Application US/08478097A
; Patent No. 6040431
;  GENERAL INFORMATION:
;    APPLICANT:  KECK, PETER
;    APPLICANT:  SMART, JOHN
;    TITLE OF INVENTION:  SINGLE-CHAIN ANALOGS OF TGF-B
;    TITLE OF INVENTION:  SUPERFAMILY (MORPHONS)
;    NUMBER OF SEQUENCES:  45
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  PATENT ADMINISTRATOR; TESTA, HURWITZ &
;      ADDRESSEE:  THIBEAULT, LLP
;      STREET:  125 HIGH STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/478,097A
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PITCHER ESQ, EDMUND R
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-080
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-248-7000
;      TELEFAX:  617-248-7100
;  INFORMATION FOR SEQ ID NO:  37:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1392 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..1392
;      OTHER INFORMATION:  /product= "MODIFIED OP-1 DNA"
US-08-478-097A-37


  Query Match             3.1%;  Score 49.4;  DB 3;  Length 1392;
  Best Local Similarity   47.6%;  Pred. No. 0.027;
  Matches  146;  Conservative    0;  Mismatches  161;  Indels    0;  Gaps    0;

Qy      84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
           ||| ||||  | | |||  |    | ||  ||||  | | | | ||  |   ||  |||
Db     695 GCTGGTGTTTGACATCACAGCCACCAGCAACCACTGGGTGGTCAATCCGCGGCACAACCT 754

Qy     144 gcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtggg 203
           |  |  | ||  |  |  |||| |||||||   |  ||      | | || | ||| |||
Db     755 GGGCCTGCAGCTCTCGGTGGAGACGCTGGATGGGCAGAGCATCAACCCCAAGTTGGCGGG 814

Qy     204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
           | | ||    | || |     |   |   || | ||| |||| |       | | ||   |
Db     815 CCTGATTGGGCGGCACGGGCCCCAGAACAAGCAGCCCTTCATGGTGGCTTTCTTCAAGGC 874

Qy     264 cgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccag 323
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Db     875 CACGGAGGTCCACTTCCGCAGCATCCGGTCCACGGGGAGCAAACAGCGCAGCCAGAACCG 934

Qy     324 caagtacgttgactactgcccggagggcaaggtggcgctcatgtccacgggcagcttgca 383
           |    |       | |   || ||| | |  |  |  |  |  ||    | ||| |     |
Db     935 CTCCAAGACGCCCAAGAACCAGGAAGCCCTGCGGATGGCCAACAGCCCGGCCGAGCGGGC 994

Qy     384 ccagctg 390
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RESULT  13
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; Sequence 42, Application US/08717294
; Patent No. 6114148
;  GENERAL INFORMATION:
;    APPLICANT:  SEED, BRIAN
;    APPLICANT:  HAAS, JURGEN
;    TITLE OF INVENTION:  HIGH LEVEL EXPRESSION OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Clark & Elbing LLP
;      STREET:  176 Federal Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,294
;      FILING DATE:  20-SEP-1996
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elbing, Karen L
;      REGISTRATION NUMBER:  35,238
;      REFERENCE/DOCKET NUMBER:  00786/345001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-428-0200
;      TELEFAX:  617-428-7045
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  42:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4451 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-717-294-42


  Query Match             3.0%;  Score 47.6;  DB 3;  Length 4451;
  Best Local Similarity   45.1%;  Pred. No. 0.09;
  Matches  176;  Conservative    0;  Mismatches  214;  Indels    0;  Gaps    0;

Qy      13 aaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttc 72
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Db    4042 AACATGTTGGTGAAGTAGCTGGAGGCGGTGATCTGGGCGTCGCTGATGGCCTTGCTCTCC 3983

Qy      73 gccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattgg 132
              ||| ||   |  ||    |  ||| |   ||   | ||  |    |  ||    |
Db    3982 ATGCCCAGGGGCATGCTGCAGCTGTTCAGGTCGCAGCCCATCAGCTCCATGCGCAGGGTG 3923

Qy     133 ttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctc 192
           | | |   | | |   |  ||      ||  |  |  |  |  ||||| || || | |
Db    3922 CTGCGGATGCTGTAGTGGGTGGGGTGCAGGCGGATGTAGCGGGCGATGATGGGGGGGTTG 3863

Qy     193 atgctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaag 252
           | | || || |||| ||  | |||||   ||   |  || || || ||||||  |    |
Db    3862 AAGATGTTGTGCTTGATGCCGCTGCTGTCCACGTTGCCGAAGAACACCATCAGGGTGCCG 3803
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Qy     253 atatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggc 312
           |    |  |   | | |  | || || ||  | |  |  ||  |   |    |  |
Db    3802 GTGCTGTTGCCGCGGTAGGTCTGCCACTTCTTGCCGTCTAGAGAGTACATGATGATGAAC 3743

Qy     313 cgcaagcccagcaagtacgttgactactgcccggagggcaaggtggcgctcatgtccacg 372
           |   |     || |    |  ||| ||| | || |  |  |||   | |   ||  | |
Db    3742 TGGCTGATGTACAGGCTGCTGAACTTCTGGCGGGCGCCCTGGGTCTTGATGCCGTGGATG 3683

Qy     373 ggcagcttgcaccagctgcacgtcttcatc 402
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RESULT  14
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; Sequence 10, Application US/07841646
; Patent No. 5266683
;  GENERAL INFORMATION:
;    APPLICANT:  OPPERMANN, HERMANN
;    APPLICANT:  OZKAYNAK, ENGIN
;    APPLICANT:  KUBERASAMPATH, THANGAVEL
;    APPLICANT:  RUEGER, DAVID C.
;    APPLICANT:  PANG, ROY H.L.
;    TITLE OF INVENTION:  OSTEOGENIC DEVICES
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  53 STATE STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  U.S.A.
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/841,646
;      FILING DATE:  19920221
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 810,560
;      FILING DATE:  20-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 827,052
;      FILING DATE:  28-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 660,162
;      FILING DATE:  22-FEB-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 621,988
;      FILING DATE:  04-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 621,849
;      FILING DATE:  04-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 616,374
;      FILING DATE:  21-NOV-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 600,024
;      FILING DATE:  18-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 599,543
;      FILING DATE:  18-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 579,865
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 569,920
;      FILING DATE:  20-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 483,913
;      FILING DATE:  22-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 422,613
;      FILING DATE:  17-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 315,342
;      FILING DATE:  23-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 232,630
;      FILING DATE:  15-AUG-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 179,460
;      FILING DATE:  08-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PITCHER, EDMUND R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-001CP6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/248-7000
;      TELEFAX:  617/248-7100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1004 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..951
;      OTHER INFORMATION:  /function= "OSTEOGENIC PROTEIN"
;      OTHER INFORMATION:  /product= "OP1B"
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US-07-841-646-10


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  Matches  135;  Conservative    0;  Mismatches  146;  Indels    0;  Gaps    0;

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Db     327 GCTGGTGTTTGACATCACAGCCACCAGCAACCACTGGGTGGTCAATCCGCGGCACAACCT 386

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Db     387 GGGCCTGCAGCTCTCGGTGGAGACGCTGGATGGGCAGAGCATCAACCCCAAGTTGGCGGG 446

Qy     204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
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Qy     264 cgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccag 323
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Db     507 CACGGAGGTCCACTTCCGCAGCATCCGGTCCACGGGGAGCAAACAGCGCAGCCAGAACCG 566

Qy     324 caagtacgttgactactgcccggagggcaaggtggcgctca 364
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RESULT  15
US-08-147-023-10
; Sequence 10, Application US/08147023
; Patent No. 5468845
;  GENERAL INFORMATION:
;    APPLICANT:  OPPERMANN, HERMANN
;    APPLICANT:  OZKAYNAK, ENGIN
;    APPLICANT:  KUBERASAMPATH, THANGAVEL
;    APPLICANT:  RUEGER, DAVID C.
;    APPLICANT:  PANG, ROY H.L.
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;    TITLE OF INVENTION:  OSTEOGENIC DEVICES
;    NUMBER OF SEQUENCES:  33
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  TESTA, HURWITZ & THIBEAULT
;      STREET:  53 STATE STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  U.S.A.
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/147,023
;      FILING DATE:  21-FEB-1992
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 810,560
;      FILING DATE:  20-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 827,052
;      FILING DATE:  28-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 660,162
;      FILING DATE:  22-FEB-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 621,988
;      FILING DATE:  04-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 621,849
;      FILING DATE:  04-DEC-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 616,374
;      FILING DATE:  21-NOV-1990
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;      APPLICATION NUMBER:  US 600,024
;      FILING DATE:  18-OCT-1990
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;      APPLICATION NUMBER:  US 599,543
;      FILING DATE:  18-OCT-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 579,865
;      FILING DATE:  07-SEP-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 569,920
;      FILING DATE:  20-AUG-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 483,913
;      FILING DATE:  22-FEB-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 422,613
;      FILING DATE:  17-OCT-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 315,342
;      FILING DATE:  23-FEB-1989
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 232,630
;      FILING DATE:  15-AUG-1988
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 179,460
;      FILING DATE:  08-APR-1988
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PITCHER, EDMUND R.
;      REGISTRATION NUMBER:  27,829
;      REFERENCE/DOCKET NUMBER:  CRP-001CP6
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617/248-7000
;      TELEFAX:  617/248-7100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1004 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  YES
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..951
;      OTHER INFORMATION:  /function= "OSTEOGENIC PROTEIN"
;      OTHER INFORMATION:  /product= "OP1B"
;      OTHER INFORMATION:  /note= "OP1B - FUSION"
US-08-147-023-10


  Query Match             3.0%;  Score 47.4;  DB 1;  Length 1004;
  Best Local Similarity   48.0%;  Pred. No. 0.069;
  Matches  135;  Conservative    0;  Mismatches  146;  Indels    0;  Gaps    0;

Qy      84 gctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccg 143
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Db     327 GCTGGTGTTTGACATCACAGCCACCAGCAACCACTGGGTGGTCAATCCGCGGCACAACCT 386

Qy     144 gcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtggg 203
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Db     387 GGGCCTGCAGCTCTCGGTGGAGACGCTGGATGGGCAGAGCATCAACCCCAAGTTGGCGGG 446

Qy     204 cttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctc 263
           | | ||    | || |      |   |   || | ||| |||| |      | | ||   |
Db     447 CCTGATTGGGCGGCACGGGCCCCAGAACAAGCAGCCCTTCATGGTGGCTTTCTTCAAGGC 506

Qy     264 cgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagcccag 323
           |  ||| | |  |  |  ||     |  | || | |  |||   || || || ||  | |
Db     507 CACGGAGGTCCACTTCCGCAGCATCCGGTCCACGGGGAGCAAACAGCGCAGCCAGAACCG 566

Qy     324 caagtacgttgactactgcccggagggcaaggtggcgctca 364
           |    |      | |   || ||| | |  |  |  |  ||
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GenCore version 4.5

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1600.4	99.9	1917	19	AAV35026	Hordeum vulgare ML
3	1316.8	82.2	1868	20	AAZ30409	Wheat Mlo fungal r
4	1316.8	82.2	1868	22	AAF24583	Nucleotide sequenc
5	1315.2	82.1	1711	21	AAA52715	Wheat Mlo homologu
6	1314.8	82.1	1692	20	AAZ30410	Wheat Mlo fungal r
7	1314.8	82.1	1693	22	AAF24584	Nucleotide sequenc
8	1305.6	81.5	1886	20	AAZ30411	Wheat Mlo fungal r
9	1305.6	81.5	1886	22	AAF24585	Nucleotide sequenc
10	936.8	58.5	1635	19	AAV35030	Hordeum vulgare ML
11	765.6	47.8	1611	19	AAV35028	Oryza sativa MLO g
12	573	35.8	2425	19	AAV35025	Hordeum vulgare ML
13	569.8	35.6	678	21	AAA52707	Wheat Mlo homologu
14	493.4	30.8	563	21	AAA52704	Soybean Mlo homolo
15	425.2	26.5	1815	21	AAZ49564	Maize MLO6 protein
16	425.2	26.5	1851	20	AAX58274	Zea mays SCLBr pro
17	379	23.7	2030	21	AAZ49561	Maize MLO2 protein
18	368.6	23.0	845	21	AAZ49560	Maize MLO1 protein
19	329	20.5	2197	20	AAZ30412	Arabidopsis thalia
20	329	20.5	2197	22	AAF24586	Nucleotide sequenc
21	312	19.5	1040	20	AAX58275	Zea mays SCLBr pro
22	298.8	18.7	1782	20	AAZ30415	Arabidopsis thalia
23	298.8	18.7	1782	22	AAF24589	Nucleotide sequenc
24	294.6	18.4	538	20	AAX58276	Zea mays SCLBr pro
25	285.8	17.8	1935	20	AAZ30413	Arabidopsis thalia
26	285.8	17.8	1935	22	AAF24587	Nucleotide sequenc
27	285.8	17.8	2148	21	AAC44660	Arabidopsis thalia
28	272	17.0	4105	19	AAV35029	Hordeum vulgare ML
29	260.6	16.3	1938	21	AAA52705	Soybean Mlo homolo
30	239.4	14.9	2096	19	AAV35023	Hordeum vulgare ML
31	225.4	14.1	1869	21	AAZ50126	Maize MLO3 cDNA.
32	225.4	14.1	1869	22	AAS01109	Maize monogenic di
33	219.6	13.7	1666	21	AAA52718	Wheat Mlo homologu
34	216.6	13.5	1725	20	AAX58270	Zea mays SCLBr pro
35	216.6	13.5	1798	21	AAZ49566	Maize MLO8 protein
36	214.2	13.4	1496	21	AAA52708	Wheat Mlo homologu
37	213	13.3	1745	21	AAA52703	Soybean Mlo homolo
38	198.8	12.4	1811	20	AAZ30414	Arabidopsis thalia
39	198.8	12.4	1811	22	AAF24588	Nucleotide sequenc
40	198.8	12.4	1880	19	AAV35031	Arabidopsis thalia
41	178.6	11.1	1660	21	AAZ49565	Maize MLO7 protein
42	161.2	10.1	513	21	AAA52702	Rice Mlo homologue
43	161	10.0	960	21	AAA52713	Soybean Mlo homolo
44	150.4	9.4	1831	20	AAX58273	Zea mays SCLBr pro
45	148.8	9.3	1841	21	AAZ49562	Maize MLO4 protein

ALIGNMENTS

RESULT 1
AAV35022
ID AAV35022 standard; DNA; 1602 BP.
XX
AC AAV35022;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare cv. Ingrid MLO gene.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS Hordeum vulgare.
XX
FH Key Location/Qualifiers
FT CDS 1..1602
FT /*tag= a
FT /product= MLO protein
XX
PN WO9804586-A2.
XX
PD 05-FEB-1998.
XX
PF 29-JUL-1997; 97WO-GB02046.
XX
PR 07-MAR-1997; 97GB-0004789.
PR 29-JUL-1996; 96GB-0015879.
PR 30-OCT-1996; 96GB-0022626.
XX
PA (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI Bueschges R, Panstruga R, Schulzelefert PMJ;

XX
DR WPI; 1998-159149/14.
DR P-PSDB; AAW59442.
XX
PT New isolated Mlo gene of barley - used to develop products for the
PT production of transgenic plants which have increased pathogen
PT resistance
XX
PS Claim 2; Fig 2; 150pp; English.
XX
CC The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC regulatory function on a pathogen defence response, such that mutants
CC exhibit a defence response in the absence of pathogen. Down-regulation
CC or out-competition of Mlo function may be used to stimulate a defence
CC response in transgenic plants conferring increased pathogen resistance,
CC especially resistance to powdery mildew or rust. The product can also
CC be used for identifying compounds able to stimulate a defence response
CC in a plant by interaction with encoded polypeptide.
XX
SQ Sequence 1602 BP; 336 A; 488 C; 466 G; 312 T; 0 other;

Query Match 100.0%; Score 1602; DB 19; Length 1602;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1602; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      61 gcggtggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaag 120
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Qy     121 ctcggccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatg 180
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Qy     181 aaggcggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggacccc 240
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Qy     241 atcatcgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgc 300
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Qy     301 ggcaccgagggccgcaagcccagcaagtacgttgactactgcccggagggcaaggtggcg 360
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Qy     481 aaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggttc 540
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Qy     601 atcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactac 660
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Qy     781 ccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctc 840
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Qy     841 atctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatg 900
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RESULT 2
AAV35026
ID AAV35026 standard; cDNA; 1917 BP.
XX
AC AAV35026;
XX
DT 13-OCT-1998 (first entry)
XX
DE Hordeum vulgare MLO gene.
XX
KW Barley; MLO; mildew; pathogen; resistance; ss.

```
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OS   Hordeum vulgare.
XX
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FT                   /product= MLO protein
FT   polyA_signal    1890..1895
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XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;    97WO-GB02046.
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PR   07-MAR-1997;    97GB-0004789.
PR   29-JUL-1996;    96GB-0015879.
PR   30-OCT-1996;    96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   P-PSDB; AAW59443.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Disclosure; Fig 7; 150pp; English.
XX
CC   The sequence is that of the MLO gene, wild-type Mlo exerts a negative
CC   regulatory function on a pathogen defence response, such that mutants
CC   exhibit a defence response in the absence of pathogen.  Down-regulation
CC   or out-competition of Mlo function may be used to stimulate a defence
CC   response in transgenic plants conferring increased pathogen resistance,
CC   especially resistance to powdery mildew or rust. The product can also
CC   be used for identifying compounds able to stimulate a defence response
CC   in a plant by interaction with encoded polypeptide.
XX
SQ   Sequence 1917 BP; 395 A; 575 C; 554 G; 393 T; 0 other;

  Query Match             99.9%;  Score 1600.4;  DB 19;  Length 1917;
  Best Local Similarity   99.9%;  Pred. No. 0;
  Matches 1601;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

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Qy    1381 tcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcg 1440
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Qy   1501 ccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaa 1560

Db   1725 ccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaa 1784

Qy   1561 gccgacatccccagtgcagatttttccttcagccagggatga 1602

Db   1785 gccgacatccccagtgcagatttttccttcagccagggatga 1826
```

RESULT 3
AAZ30409
ID AAZ30409 standard; DNA; 1868 BP.
XX
AC AAZ30409;
XX
DT 21-DEC-1999 (first entry)
XX
DE Wheat Mlo fungal resistance gene TrMlo1.
XX
KW Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW Mlo; Erysiphe graminis; powdery mildew; ss.
XX
OS Triticum sp.
XX
FH Key Location/Qualifiers
FT CDS 176..1780
FT /*tag= a
FT /product= "fungal resistance protein Mlo1"
XX
PN WO9947552-A2.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99WO-EP01779.
XX
PR 17-MAR-1998; 98US-0042763.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM;
XX
DR WPI; 1999-571820/48.
DR P-PSDB; AAY26966.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 58-60; 102pp; English.
XX
CC This sequence represents the coding region for the wheat fungal
CC resistance gene TrMlo1. The Mlo protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carbohydrate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new Mlo sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).
XX
SQ Sequence 1868 BP; 399 A; 565 C; 521 G; 383 T; 0 other;

Query Match 82.2%; Score 1316.8; DB 20; Length 1868;
Best Local Similarity 90.3%; Pred. No. 4.8e-271;
Matches 1431; Conservative 0; Mismatches 147; Indels 6; Gaps 2;

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Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81

Db    200 ccagcgaggacgctgccggagacgccgtcctgggcggtggccctcgtcttcgccgtcatg 259

Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141

Db    260 atcatcgtgtccgtcctcctggagcacgcgctccataagctcggccattggttccacaag 319

Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201

Db    320 cggcacaagaacgcgctggcggaggcgctggagaagatcaaggcggagctcatgctggtg 379

Qy    202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261

Db    380 ggcttcatctcgctgctgctcgccgtgacgcaggaccc---catctccgggatatgcatc 436

Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321

Db    437 tccgagaaggccgccagcatcatgcggccctgcaagctgccccctggctccgtcaagagc 496

Qy    322 agcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcagc 378

Db    497 aagtacaaagactactactgcgccaaacagggcaaggtgtcgctcatgtccacgggcagc 556

Qy    379 ttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtc 438

Db    557 ttgcaccagctgcacatattcatcttcgtgctcgccgtcttccatgtcacctacagcgtc 616

Qy    439 atcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagacc 498

Db    617 atcatcatggctctaagccgtctcaaaatgagaacctggaagaaatgggagacagagacc 676

Qy    499 acctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacg 558

Db    677 gcctccctggaataccagttcgcaaatgatcctgcgcggttccgcttcacgcaccagacg 736

Qy    559 tcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatgggtggtggcc 618

Db    737 tcgttcgtgaagcggcacctgggcctctccagcacccccggcgtcagatgggtggtggcc 796

Qy    619 ttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggc 678

Db    797 ttcttcaggcagttcttcaggtcggtcaccaaggtggactacctcaccttgagggcaggc 856

Qy    679 ttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagagg 738

Db    857 ttcatcaacgcgcatttgtcgcataacagcaagttcgacttccacaagtacatcaagagg 916

Qy    739 tcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcg 798

Db    917 tccatggaggacgacttcaaagtcgtcgttggcatcagcctcccgctgtggtgtgtggcg 976

Qy    799 atcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatc 858

Db    977 atcctcaccctcttccttgacattgacgggatcggcacgctcacctggatttctttcatc 1036

Qy    859 cctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggcc 918

Db   1037 cctctcgtcatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggcc 1096

Qy    919 ctggagatccaggaccgggcgagcgtcatcaaggggcccccgtggtcgagcccagcaac 978

Db   1097 ctggagatccaggaccgggcgagcgtcatcaaggggcgcccgtggttgagcccagcaac 1156

Qy    979 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttc 1038

Db   1157 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgctattc 1216

Qy   1039 cagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaa 1098

Db   1217 cagaacgcgtttcagatggcacatttcgtgtggacagtggccacgcccggcttgaagaaa 1276

Qy   1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158

Db   1277 tgcttccatatgcacatcgggctgagcatcatgaaggtcgtgctggggctggctcttcag 1336
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```
Qy   1159 ttcctctgcagctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaac 1218
          |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db   1337 ttcctctgcagctatatcaccttcccgctctacgcgctcgtcacacagatgggatcaaac 1396

Qy   1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
          |||||||||||||||||||||||||||||| |||||||||| || ||||||||||||||||
Db   1397 atgaagaggtccatcttcgacgagcagacggccaaggcgctgacaaactggcggaacacg 1456

Qy   1279 gccaaggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgac 1338
          |||||||||||||||| |||||||||||||||||||||||||| ||||||||||||||||
Db   1457 gccaaggagaagaagaaggtccgagacacggacatgctgatggcgcagatgatcggcgac 1516

Qy   1339 gcaacaccgagccgaggctcgtcgccgatgccgagccggggctcatcacccgtgcacctg 1398
          || || || |||||||| |||||| ||||| |||||||||| || || |||||||||
Db   1517 gcgacgcccagccgaggggcgtcgcccatgcctagccggggctcgtcgccagtgcacctg 1576

Qy   1399 cttcacaagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458
          |||||||||||||||| ||||| ||||| ||||||||| |||| |||||||||||| ||
Db   1577 cttcacaagggcatgggacggtccgacgatccccagagcacgccaacctcgccaagggcc 1636

Qy   1459 cagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaat 1518
            | ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||||
Db   1637 atggaggaggctagggacatgtacccggttgtggtggcgcatccagtgcacagactaaat 1696

Qy   1519 cctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgca 1578
          |||   |||||||| ||||| | |||||||||||| ||||| | |||||| ||||| |||
Db   1697 cctgctgacaggagaaggtcggtctcgtcgtcggcactcgatgtcgacattcccagcgca 1756

Qy   1579 gatttttccttcagccagggatga 1602
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Db   1757 gatttttccttcagccagggatga 1780
```

```
RESULT   4
AAF24583
ID   AAF24583 standard; DNA; 1868 BP.
XX
AC   AAF24583;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of the wheat Mlo protein TrMlo1.
XX
KW   Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW   powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             176..1780
FT                   /*tag= a
FT                   /product= "Mlo protein"
XX
PN   WO200078799-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-EP05576.
XX
PR   18-JUN-1999;   99US-0336112.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM,  Wang HX;
PI   Vernooij BT,  Levin JZ,  Heifetz PB,  Patton DA,  Que Q;
XX
DR   WPI; 2001-112311/12.
DR   P-PSDB; AAB31250.
XX
PT   Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT   producing fungal resistant plants, in particular wheat plant  -
XX
PS   Claim 2; Page 88-90; 128pp; English.
XX
CC   The present sequence encodes a Mlo protein. Mlo proteins given
CC   resistance to fungal pathogens which infect living epidermal plant cells.
CC   Mlo proteins give proteins resistance to fungal pathogens, especially
CC   Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC   locus are responsible for a plant resistant pathotype. The mechanism
CC   of Mlo resistance involves the formation of large cell wall appositions,
CC   called papillae, at pathogen contact sites. Papillae mainly contain
CC   callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC   encoding Mlo proteins are useful for making transgenic plants,
CC   preferably wheat, which are resistant to fungal pathogens.
XX
SQ   Sequence 1868 BP; 399 A; 565 C; 521 G; 383 T; 0 other;
```

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  Query Match             82.2%;  Score 1316.8;  DB 22;  Length 1868;
  Best Local Similarity   90.3%;  Pred. No. 4.8e-271;
  Matches 1431;  Conservative    0;  Mismatches  147;  Indels    6;  Gaps    2;

Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
          || ||| ||  |||||||||||||||||||||||||||  | |||||||||| ||||
Db    200 ccagcgaggacgctgccggagacgccgtcctgggcggtggccctcgtcttcgccgtcatg 259

Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
            |  |||||||||||||| |||| |||  ||||| |||||||||||||||||||  |
Db    260 atcatcgtgtccgtcctcctggagcacgcgctccataagctcggccattggttccacaag 319

Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
          |||||||||||  || |||  |||||||||||||||||| ||||||||||||||||||||
Db    320 cggcacaagaacgcgctggcggaggcgctggagaagatcaaggcggagctcatgctggtg 379

Qy    202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261
          |||||||| || ||||| |||  ||| ||||||||||   |||| ||  ||||||||||
Db    380 ggcttcatctcgctgctgctcgccgtgacgcaggaccc---catctccgggatatgcatc 436

Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
          ||||||  | ||||||  | |||||  |||||||||||||    | | |    |  ||||  |
Db    437 tccgagaaggccgccagcatcatgcggccctgcaagctgccccctggctccgtcaagagc 496

Qy    322 agcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcagc 378
          |   |  | |   |||||||| |     |||||||||||| ||||||||||||||||||||
Db    497 aagtacaaagactactactgcgccaaacagggcaaggtgtcgctcatgtccacgggcagc 556

Qy    379 ttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtc 438
          |||||||||||||||  | |||||||||||||||||  ||||||||||||||||||||||||
Db    557 ttgcaccagctgcacatattcatcttcgtgctcgccgtcttccatgtcacctacagcgtc 616

Qy    439 atcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagacc 498
          |||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    617 atcatcatggctctaagccgtctcaaaatgagaacctggaagaaatgggagacagagacc 676

Qy    499 acctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacg 558
          |||||| |||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db    677 gcctccctggaataccagttcgcaaatgatcctgcgcggttccgcttcacgcaccagacg 736

Qy    559 tcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatgggtggtggcc 618
          |||||||||||||| ||||||||||||||||||||||||| ||| ||||||||||||||||
Db    737 tcgttcgtgaagcggcacctgggcctctccagcacccccggcgtcagatgggtggtggcc 796

Qy    619 ttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggc 678
          |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db    797 ttcttcaggcagttcttcaggtcggtcaccaaggtggactacctcaccttgagggcaggc 856

Qy    679 ttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagagg 738
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    857 ttcatcaacgcgcatttgtcgcataacagcaagttcgacttccacaagtacatcaagagg 916

Qy    739 tcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcg 798
          || |||||||||||||||| |||||||| |||||||||||||||||||| ||||||||
Db    917 tccatggaggacgacttcaaagtcgtcgttggcatcagcctcccgctgtggtgtgtggcg 976
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Qy    799 atcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatc 858
Db    977 atcctcaccctcttccttgacattgacgggatcggcacgctcacctggatttctttcatc 1036

Qy    859 cctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggcc 918
Db   1037 cctctcgtcatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggcc 1096

Qy    919 ctggagatccaggaccgggcgagcgtcatcaaggggggcccccgtggtcgagcccagcaac 978
Db   1097 ctggagatccaggaccgggcgagcgtcatcaaggggcgcccgtggttgagcccagcaac 1156

Qy    979 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttc 1038
Db   1157 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgctattc 1216

Qy   1039 cagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaa 1098
Db   1217 cagaacgcgtttcagatggcacatttcgtgtggacagtggccacgcccggcttgaagaaa 1276

Qy   1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158
Db   1277 tgcttccatatgcacatcgggctgagcatcatgaaggtcgtgctggggctggctcttcag 1336

Qy   1159 ttcctctgcagctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaac 1218
Db   1337 ttcctctgcagctatatcaccttcccgctctacgcgctcgtcacacagatgggatcaaac 1396

Qy   1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
Db   1397 atgaagaggtccatcttcgacgagcagacggccaaggcgctgacaaactggcggaacacg 1456

Qy   1279 gccaaggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgac 1338
Db   1457 gccaaggagaagaagaaggtccgagacacggacatgctgatggcgcagatgatcggcgac 1516

Qy   1339 gcaacaccgagccgaggctcgtcgccgatgccgagccggggctcatcacccgtgcacctg 1398
Db   1517 gcgacgcccagccgaggggcgtcgcccatgcctagccggggctcgtcgccagtgcacctg 1576

Qy   1399 cttcacaagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458
Db   1577 cttcacaagggcatgggacggtccgacgatccccagagcacgccaacctcgccaagggcc 1636

Qy   1459 cagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaat 1518
Db   1637 atggaggaggctagggacatgtacccggttgtggtggcgcatccagtgcacagactaaat 1696

Qy   1519 cctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgca 1578
Db   1697 cctgctgacaggagaaggtcggtctcgtcgtcggcactcgatgtcgacattcccagcgca 1756

Qy   1579 gatttttccttcagccagggatga 1602
Db   1757 gatttttccttcagccagggatga 1780


RESULT   5
AAA52715
ID   AAA52715 standard; cDNA; 1711 BP.
XX
AC   AAA52715;
XX
DT   27-OCT-2000  (first entry)
XX
DE   Wheat Mlo homologue putative coding sequence #4.
XX
KW   Wheat; Mlo homologue; disease resistance; ss.
XX
OS   Triticum aestivum.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1605
FT                   /*tag= a
FT                   /product= "Mlo homologue"
XX
PN   WO200036110-A2.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US30181.
XX
PR   18-DEC-1998;   98US-0112737.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE,  Miao G,  Rafalski JA,  Fang Y,  Sakai H,  Taramino G;
XX
DR   WPI; 2000-431590/37.
DR   P-PSDB; AAB01805.
XX
PT   New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT   creating transgenic plants with altered levels of disease resistance -
XX
PS   Claim 2; Page 64; 79pp; English.
XX
CC   The present sequence is a putative coding sequence for a Mlo homologue
CC   from wheat. It was identified by searching a root and leaf cDNA library
CC   for sequences encoding proteins similar to Mlo from Hordeum vulgare
CC   (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
CC   graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC   priming of disease resistance even if the pathogen is not present. The
CC   gene and protein can be used to create transgenic plants which have
CC   increased disease resistance, as well as allowing researchers to find
CC   other resistance-conferring genes and proteins.
XX
SQ   Sequence 1711 BP; 377 A; 505 C; 473 G; 356 T; 0 other;


  Query Match           82.1%;  Score 1315.2;  DB 21;  Length 1711;
  Best Local Similarity  89.8%;  Pred. No. 1e-270;
  Matches 1436;  Conservative    0;  Mismatches  158;  Indels    6;  Gaps    2;

Qy      6 ggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggt 65
Db      9 ggactacgagtacccccggcgcggacgctgccggagacgccgtcctgggcggtggcgct 68

Qy     66 ggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcgg 125
Db     69 cgtcttcgccgtcatgatcatcgtgtccgtcctcctggagcacgcgctccacaagctcgg 128

Qy    126 ccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggc 185
Db    129 ccattggttccacaagcggcacaagaacgcgctggcggaggcgctggagaagatcaaagc 188

Qy    186 ggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcat 245
Db    189 ggagctgatgctggtggggttcatctcgctgctgctcgccgtgacgcaggaccc---aat 245

Qy    246 cgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcac 305
Db    246 ctccgggatatgcatctccgagaaggccgccagcatcatgcggccctgcagcctgccccc 305

Qy    306 cgagggccgcaagcccagcaagtacgttgactactgccc---ggagggcaaggtggcgct 362
Db    306 tggttccgtcaagagcaagtacaaagactactactgcgccaaaaagggcaaggtgtcgct 365

Qy    363 catgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttcca 422
Db    366 aatgtccacgggcagcttgcaccagctccacatattcatcttcgtgctcgccgtcttcca 425

Qy    423 tgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaagaa 482
Db    426 tgtcacctacagcgtcatcatcatggctctaagccgtctcaaaatgaggacatggaagaa 485

Qy    483 atgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggttccg 542
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Db    486 atgggagacagagaccgcctccttggaataccagttcgcaaatgatcctgcgcggttccg 545

Qy    543 gttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctggcat 602
Db    546 cttcacgcaccagacgtcgttcgtgaagcggcacctgggcctctccagcacccccggcat 605

Qy    603 cagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactacct 662
Db    606 cagatgggtggtggccttcttcaggcagttcttcaggtcggtcaccaaggtggactacct 665

Qy    663 gaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttcca 722
Db    666 caccctgagggcaggcttcatcaacgcgcatttgtcgcataacagcaagttcgacttcca 725

Qy    723 caagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctccc 782
Db    726 caagtacatcaagaggtccatggaggacgacttcaaagtcgtcgttggcatcagcctccc 785

Qy    783 gctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctcat 842
Db    786 gctgtggtgtgtggcgatcctcaccctcttccttgatattgacgggatcggcacgctcac 845

Qy    843 ctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatgat 902
Db    846 ctggatttctttcatccctctcgtcatcctcttgtgtgttggaaccaagctggagatgat 905

Qy    903 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcccccgt 962
Db    906 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcgcccgt 965

Qy    963 ggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1022
Db    966 ggttgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1025

Qy   1023 acacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccac 1082
Db   1026 acacctgacgctgttccagaatgcgtttcagatggcacatttcgtctggacagtggccac 1085

Qy   1083 gcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggt 1142
Db   1086 gcccggcttgaagaaatgcttccatatgcacatcggtctgagcatcatgaaggtcgtgct 1145

Qy   1143 ggggctagctctccagttcctctgcagctatatgaccttcccctctacgcgctcgtcac 1202
Db   1146 ggggctggctcttcagttcctctgcagctatatcaccttcccctctacgcgctcgtcac 1205

Qy   1203 acagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcac 1262
Db   1206 acagatgggatcgaacatgaagaggtccatcttcgacgagcagacggccaaggcgctgac 1265

Qy   1263 caactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatggc 1322
Db   1266 caactggcggaacacggccaaggagaagaagaaggtccgagacacggacatgctgatggc 1325

Qy   1323 tcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggctc 1382
Db   1326 gcagatgatcggcgacgcgacgcccagccgaggcacgtcgccgatgcctagccgggcttc 1385

Qy   1383 atcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgcc 1442
Db   1386 gtcaccggtgcacctgcttcacaagggcatgggacggtccgacgatccccagagcgcgcc 1445

Qy   1443 cacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcaccc 1502
Db   1446 gacctcgccaaggaccatggaggaggctagggacatgtacccggttgtggtggcgcatcc 1505

Qy   1503 ggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagc 1562
Db   1506 cgtgcacagactaaatcctgctgacaggcggaggtcggtctcttcgtcggcactcgatgc 1565

Qy   1563 cgacatccccagtgcagatttttccttcagccagggatga 1602
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Db   1566 cgacatccccagcgcagatttttccttcagccagggatga 1605


RESULT   6
AAZ30410
ID   AAZ30410 standard; DNA; 1692 BP.
XX
AC   AAZ30410;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Wheat Mlo fungal resistance gene TrMlo2.
XX
KW   Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW   papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW   Mlo; Erysiphe graminis; powdery mildew; ss.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1605
FT                   /*tag= a
FT                   /product= "fungal resistance protein Mlo2"
FT                   /transl_except= (pos:502..504, aa;Xaa)
FT                   /note= "Xaa = unknown"
XX
PN   WO9947552-A2.
XX
PD   23-SEP-1999.
XX
PF   17-MAR-1999;   99WO-EP01779.
XX
PR   17-MAR-1998;   98US-0042763.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM;
XX
DR   WPI; 1999-571820/48.
DR   P-PSDB; AAY26967.
XX
PT   New proteins useful for generating transgenic plants resistant to
PT   fungal infection -
XX
PS   Claim 2; Page 63-65; 102pp; English.
XX
CC   This sequence represents the coding region for the wheat fungal
CC   resistance gene TrMlo2. The Mlo protein confers resistance to fungal
CC   pathogens by stimulating the formation of large cell wall appositions,
CC   designated papillae, at the contact site with the fungal pathogen.
CC   These papillae mainly contain callose, but also contain carbohydrate,
CC   phenols and proteins and are used to prevent penetration of the fungal
CC   hyphae into the plant. The new Mlo sequences are used to generate
CC   transgenic plants resistant to fungal pathogens, especially Erysiphe
CC   graminis (powdery mildew).
XX
SQ   Sequence 1692 BP; 360 A; 505 C; 471 G; 355 T; 1 other;


  Query Match             82.1%;  Score 1314.8;  DB 20;  Length 1692;
  Best Local Similarity   89.7%;  Pred. No. 1.3e-270;
  Matches 1435;  Conservative    1;  Mismatches  158;  Indels    6;  Gaps    2;

Qy       6 ggacaaaaaaggggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggt 65
Db       9 ggactacgagtacccccggcgcggacgctgccggagacgccgtcctgggcggtggcgct 68

Qy      66 ggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcgg 125
Db      69 cgtcttcgccgtcatgatcatcgtgtccgtcctcctggagcacgcgctccacaagctcgg 128

Qy     126 ccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggc 185
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Db    129 ccattggttccacaagcggcacaagaacgcgctggcggaggcgctggagaagatcaaagc 188

Qy    186 ggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggacccccatcat 245

Db    189 ggagctgatgctggtggggttcatctcgctgctgctcgccgtgacgcaggaccc---aat 245

Qy    246 cgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcac 305

Db    246 ctccgggatatgcatctccgagaaggccgccagcatcatgcggccctgcagcctgccccc 305

Qy    306 cgagggccgcaagcccagcaagtacgttgactactgccc---ggagggcaaggtggcgct 362

Db    306 tggttccgtcaagagcaagtacaaagactactactgcgccaaaaagggcaaggtgtcgct 365

Qy    363 catgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttcca 422

Db    366 aatgtccacgggcagcttgcaccagctccacatgttcatcttcgtgctcgccgtcttcca 425

Qy    423 tgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaagaa 482

Db    426 tgtcacctacagcgtcatcatcatggctctaagccgtctcaaaatgaggacatggaagaa 485

Qy    483 atgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggttccg 542

Db    486 atgggagacagagaccgyctccttggaataccagttcgcaaatgatcctgcgcggttccg 545

Qy    543 gttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctggcat 602

Db    546 cttcacgcaccagacgtcgttcgtgaagcgtcacctgggcctctccagcaccccggcat 605

Qy    603 cagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactacct 662

Db    606 cagatgggtggtggccttcttcaggcagttcttcaggtcggtcaccaaggtggactacct 665

Qy    663 gaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttcca 722

Db    666 caccctgagggcaggcttcatcaacgcgcatttgtcgcataacagcaagttcgacttcca 725

Qy    723 caagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctccc 782

Db    726 caagtacatcaagaggtccatggaggacgacttcaaagtcgtcgttggcatcagcctccc 785

Qy    783 gctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctcat 842

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Qy    843 ctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatgat 902

Db    846 ctggatttctttcatccctctcgtcatcctcttgtgtgttggaaccaagctggagatgat 905

Qy    903 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaagggggccccgt 962

Db    906 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcgcccgt 965

Qy    963 ggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1022

Db    966 ggttgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1025

Qy   1023 acacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccac 1082

Db   1026 acacctgacgctgttccagaatgcgtttcagatggcacatttcgtctggacagtggccac 1085

Qy   1083 gcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggt 1142

Db   1086 gcccggcttgaagaaatgcttccatatgcacatcggtctgagcatcatgaaggtcgtgct 1145

Qy   1143 ggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcac 1202

Db   1146 ggggctggctcttcagttcctctgcagctatatcaccttccccctctacgcgctcgtcac 1205

Qy   1203 acagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcac 1262

Db   1206 acagatgggatcgaacatgaagaggtccatcttcgacgagcagacggccaaggcgctgac 1265

Qy   1263 caactggcggaacacggccaaggagaagaagaagaaagtccgagacacggacatgctgatggc 1322

Db   1266 caactggcggaacacggccaaggagaagaagaaggtccgagacacggacatgctgatggc 1325

Qy   1323 tcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggctc 1382

Db   1326 gcagatgatcggcgacgcgacgcccagccgaggcacgtcgccgatgcctagccgggcttc 1385

Qy   1383 atcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgcc 1442

Db   1386 gtcaccggtgcacctgcttcacaagggcatgggacggtccgacgatccccagagcgcgcc 1445

Qy   1443 cacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcaccc 1502

Db   1446 gacctcgccaaggaccatggaggaggctagggacatgtacccggttgtggtggcgcatcc 1505

Qy   1503 ggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagc 1562

Db   1506 cgtgcacagactaaatcctgctgacaggcggaggtcggtctcttcgtcggcactcgatgc 1565

Qy   1563 cgacatccccagtgcagatttttccttcagccagggatga 1602

Db   1566 cgacatccccagcgcagatttttccttcagccagggatga 1605
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```
RESULT   7
AAF24584
ID   AAF24584 standard; DNA; 1693 BP.
XX
AC   AAF24584;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of the wheat Mlo protein TrMlo2.
XX
KW   Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW   powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1605
FT                   /*tag= a
FT                   /product= "Mlo protein"
FT                   /transl_except= "(pos: 502..504, aa: Xaa)"
FT                   /note= "Xaa is an unspecified amino acid"
XX
PN   WO200078799-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-EP05576.
XX
PR   18-JUN-1999;   99US-0336112.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM,  Wang HX;
PI   Vernooij BT,  Levin JZ,  Heifetz PB,  Patton DA,  Que Q;
XX
DR   WPI; 2001-112311/12.
DR   P-PSDB; AAB31251.
XX
PT   Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT   producing fungal resistant plants, in particular wheat plant  -
XX
PS   Claim 2; Page 92-94; 128pp; English.
XX
CC   The present sequence encodes a Mlo protein. Mlo proteins given
CC   resistance to fungal pathogens which infect living epidermal plant cells.
```

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CC   Mlo proteins give proteins resistance to fungal pathogens, especially
CC   Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC   locus are responsible for a plant resistant pathotype. The mechanism
CC   of Mlo resistance involves the formation of large cell wall appositions,
CC   called papillae, at pathogen contact sites. Papillae mainly contain
CC   callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC   encoding Mlo proteins are useful for making transgenic plants,
CC   preferably wheat, which are resistant to fungal pathogens.
XX
SQ   Sequence 1693 BP; 360 A; 505 C; 472 G; 355 T; 1 other;


  Query Match            82.1%;  Score 1314.8;  DB 22;  Length 1693;
  Best Local Similarity  89.7%;  Pred. No. 1.3e-270;
  Matches 1435;  Conservative    1;  Mismatches  158;  Indels    6;  Gaps    2;

Qy      6 ggacaaaaaaggggtgccggcgcgcgggagctgccggagacgccgtcgtgggcggtggcggt 65
          ||||  |  |       |||||||||  ||||||||||||||||||| ||||||||||||  |
Db      9 ggactacgagtacccccggcgcggacgctgccggagacgccgtcctgggcggtggcgct 68

Qy     66 ggtcttcgccgccatggtgctcgtgtccgtcctcatggaacacggcctccacaagctcgg 125
          |||||||||| |||| |  ||||||||||||||| |||| ||||  ||||||||||||||
Db     69 cgtcttcgccgtcatgatcatcgtgtccgtcctcctggagcacgcgctccacaagctcgg 128

Qy    126 ccattggttccagcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggc 185
          ||||||||||||  | ||||||||||| || |||  ||||||||||||||||||| || ||
Db    129 ccattggttccacaagcggcacaagaacgcgctggcggaggcgctggagaagatcaaagc 188

Qy    186 ggagctcatgctggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcat 245
          ||||||  |||||||||||  |||||  || |||||  |||  |||  ||||||||||    ||
Db    189 ggagctgatgctggtggggttcatctcgctgctgctcgccgtgacgcaggaccc---aat 245

Qy    246 cgccaagatatgcatctccgaggatgccgccgacgtcatgtggccctgcaagcgcggcac 305
          | ||  |||||||||||||||| | ||||||  | |||||  |||||||||  |    | |
Db    246 ctccgggatatgcatctccgagaaggccgccagcatcatgcggccctgcagcctgccccc 305

Qy    306 cgagggccgcaagcccagcaagtacgttgactactgccc---ggagggcaaggtggcgct 362
          |    |  ||||  ||   |  | |   ||||||||  |     |||||||||||  ||||
Db    306 tggttccgtcaagagcaagtacaaagactactactgcgccaaaaagggcaaggtgtcgct 365

Qy    363 catgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttcca 422
          |||||||||||||||||||||||||| ||| | ||||||||||||||||  |||||||||
Db    366 aatgtccacgggcagcttgcaccagctccacatgttcatcttcgtgctcgccgtcttcca 425

Qy    423 tgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaagaa 482
          |||||||||||||||||||| ||| ||||||||||||||||||||| ||||||||||
Db    426 tgtcacctacagcgtcatcatcatggctctaagccgtctcaaaatgaggacatggaagaa 485

Qy    483 atgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggttccg 542
          ||||||||||||||| :|||||||||||||||||||||||||||||||||||| ||||||||
Db    486 atgggagacagagaccgyctccttggaataccagttcgcaaatgatcctgcgcggttccg 545

Qy    543 gttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctggcat 602
          |||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db    546 cttcacgcaccagacgtcgttcgtgaagcgtcacctgggcctctccagcaccccggcat 605

Qy    603 cagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggactacct 662
          |||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db    606 cagatgggtggtggccttcttcaggcagttcttcaggtcggtcaccaaggtggactacct 665

Qy    663 gaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttcca 722
          |||  ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    666 caccctgagggcaggcttcatcaacgcgcatttgtcgcataacagcaagttcgacttcca 725

Qy    723 caagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcctccc 782
          |||||||||||||||||| |||||||||||||||||| ||||||| ||||||||||||||
Db    726 caagtacatcaagaggtccatggaggacgacttcaaagtcgtcgttggcatcagcctccc 785

Qy    783 gctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgctcat 842
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Db    786 gctgtggtgtgtggcgatcctcaccctcttccttgatattgacgggatcggcacgctcac 845

Qy    843 ctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagatgat 902
          |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db    846 ctggatttctttcatccctctcgtcatcctcttgtgtgttggaaccaagctggagatgat 905

Qy    903 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggggcccccgt 962
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    906 catcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggggcgcccgt 965

Qy    963 ggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1022
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    966 ggttgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttcttcat 1025

Qy   1023 acacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggccac 1082
          |||||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db   1026 acacctgacgctgttccagaatgcgtttcagatggcacatttcgtctggacagtggccac 1085

Qy   1083 gcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggtggt 1142
          |||||||||||||||||||| ||| | ||| ||||| ||||||||||||||||| ||| |
Db   1086 gcccggcttgaagaaatgcttccatatgcacatcggtctgagcatcatgaaggtcgtgct 1145

Qy   1143 ggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgtcac 1202
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Db   1146 ggggctggctcttcagttcctctgcagctatatcaccttccccctctacgcgctcgtcac 1205

Qy   1203 acagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctcac 1262
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Db   1206 acagatgggatcgaacatgaagaggtccatcttcgacgagcagacggccaaggcgctgac 1265

Qy   1263 caactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatggc 1322
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db   1266 caactggcggaacacggccaaggagaagaagaaggtccgagacacggacatgctgatggc 1325

Qy   1323 tcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggctc 1382
          |||||||||||||||| || || |||||||| |||||||||||| |||||||  ||
Db   1326 gcagatgatcggcgacgcgacgcccagccgaggcacgtcgccgatgcctagccgggcttc 1385

Qy   1383 atcacccgtgcacctgcttcacaagggcatgggcggtcggacgacccccagagcgcgcc 1442
          |||||  |||||||||||||||||||||||||||  |||||  |||||||||||||||
Db   1386 gtcaccggtgcacctgcttcacaagggcatgggacggtccgacgatccccagagcgcgcc 1445

Qy   1443 cacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcaccc 1502
          ||||||||||||||  | ||||||||||||||||||||||||||||||||||||| ||
Db   1446 gacctcgccaaggaccatggaggaggctagggacatgtacccggttgtggtggcgcatcc 1505

Qy   1503 ggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagc 1562
          ||||||||||||||||    |||||| ||||||| | ||| |||||||| ||||| ||
Db   1506 cgtgcacagactaaatcctgctgacaggcggaggtcggtctcttcgtcggcactcgatgc 1565

Qy   1563 cgacatccccagtgcagatttttccttcagccagggatga 1602
          |||||||||||| ||||||||||||||||||||||||||
Db   1566 cgacatccccagcgcagatttttccttcagccagggatga 1605


RESULT   8
AAZ30411
ID   AAZ30411 standard; DNA; 1886 BP.
XX
AC   AAZ30411;
XX
DT   21-DEC-1999  (first entry)
XX
DE   Wheat Mlo fungal resistance gene TrMlo3.
XX
KW   Consensus; resistance; fungus; pathogen; wheat; cell wall; apposition;
KW   papilla; contact site; callose; carbohydrate; phenol; transgenic plant;
KW   Mlo; Erysiphe graminis; powdery mildew; ss.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             198..1802
FT                   /*tag= a
FT                   /product= "fungal fusion protein Mlo3"
XX
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PN WO9947552-A2.
XX
PD 23-SEP-1999.
XX
PF 17-MAR-1999; 99WO-EP01779.
XX
PR 17-MAR-1998; 98US-0042763.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Salmeron JM, Weislo LJ, Strawn LJ, Kramer CM; .
XX
DR WPI; 1999-571820/48.
DR P-PSDB; AAY26968.
XX
PT New proteins useful for generating transgenic plants resistant to
PT fungal infection -
XX
PS Claim 2; Page 68-70; 102pp; English.
XX
CC This sequence represents the coding region for the wheat fungal
CC resistance gene TrMlo3. The Mlo protein confers resistance to fungal
CC pathogens by stimulating the formation of large cell wall appositions,
CC designated papillae, at the contact site with the fungal pathogen.
CC These papillae mainly contain callose, but also contain carbohydrate,
CC phenols and proteins and are used to prevent penetration of the fungal
CC hyphae into the plant. The new Mlo sequences are used to generate
CC transgenic plants resistant to fungal pathogens, especially Erysiphe
CC graminis (powdery mildew).
XX
SQ Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

Query Match 81.5%; Score 1305.6; DB 20; Length 1886;
Best Local Similarity 89.9%; Pred. No. 1.2e-268;
Matches 1424; Conservative 0; Mismatches 154; Indels 6; Gaps 2;

```
Qy     22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
Db    222 ccggcgcggacgctgccggagacgccgtcctgggcggtggcgctggtcttcgccgtcatg 281

Qy     82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
Db    282 atcatcgtctccgtcctcctggagcacgcgctccacaagctcggccattggttccacaag 341

Qy    142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
Db    342 cggcacaagaacgcgctggcggaggcgctggagaagatgaaggcggagctgatgctggtg 401

Qy    202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261
Db    402 ggattcatctcgctgctgctcgccgtcacgcaggaccc---aatctccgggatatgcatc 458

Qy    262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
Db    459 tcccagaaggccgccagcatcatgcgcccctgcaaggtggaacccggttccgtcaagagc 518

Qy    322 agcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcagc 378
Db    519 aagtacaaggactactactgcgccaaagagggcaaggtggcgctcatgtccacgggcagc 578

Qy    379 ttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtc 438
Db    579 ctgcaccagctccacatattcatcttcgtgctagccgtcttccatgtcacctacagcgtc 638

Qy    439 atcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagacc 498
Db    639 atcatcatggctctaagccgtctcaagatgagaacatggaagaaatgggagacagaaacc 698

Qy    499 acctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacg 558
Db    699 gcctccttggaataccagttcgcaaatgatcctgcgcggttccgcttcacgcaccagacg 758

Qy    559 tcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatgggtggtggcc 618
Db    759 tcgttcgtgaagcggcacctgggcctgtccagcacccccggcgtcagatgggtggtggcc 818

Qy    619 ttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggc 678
Db    819 ttcttcaggcagttcttcaggtcggtcaccaaggtggactacctcaccttgagggcaggc 878

Qy    679 ttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagagg 738
Db    879 ttcatcaacgcgcacttgtcgcagaacagcaagttcgacttccacaagtacatcaagagg 938

Qy    739 tcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcg 798
Db    939 tccatggaggacgacttcaaagtcgtcgttggcatcagcctcccgctgtgggctgtggcg 998

Qy    799 atcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatc 858
Db    999 atcctcaccctcttccttgatatcgacgggatcggcacactcacctgggtttctttcatc 1058

Qy    859 cctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggcc 918
Db   1059 cctctcatcatcctcttgtgtgttggaaccaagctagagatgatcatcatggggatggcc 1118

Qy    919 ctggagatccaggaccgggcgagcgtcatcaaggggcccccgtggtcgagcccagcaac 978
Db   1119 ctggagatccaggaccggtcgagcgtcatcaaggggcacccgtggtcgagcccagcaac 1178

Qy    979 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttc 1038
Db   1179 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgctgttc 1238

Qy   1039 cagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaa 1098
Db   1239 cagaacgcgtttcagatggcacatttcgtgtggacagtggccacgcccggcttgaaggac 1298

Qy   1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158
Db   1299 tgcttccatatgaacatcgggctgagcatcatgaaggtcgtgctggggctggctctccag 1358

Qy   1159 ttcctctgcagctatatgaccttccccctctacgcgctcgtcacacagatgggatcaaac 1218
Db   1359 ttcctgtgcagctacatcaccttccccctctacgcgctagtcacacagatgggatcaaac 1418

Qy   1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
Db   1419 atgaagaggtccatcttcgacgagcagacagccaaggcgctgaccaactggcggaacacg 1478

Qy   1279 gccaaggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgac 1338
Db   1479 gccaaggagaagaagaaggtccgagacacggacatgctgatggcgcagatgatcggcgac 1538

Qy   1339 gcaacaccgagccgaggctcgtcgccgatgccgagccggggctcatcacccgtgcacctg 1398
Db   1539 gcaacacccagccgaggcacgtccccgatgcctagccggggctcatcgccggtgcacctg 1598

Qy   1399 cttcacaagggcatggggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458
Db   1599 cttcagaagggcatgggacggtctgacgatccccagagcgcaccgacctcgccaaggacc 1658

Qy   1459 cagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaat 1518
Db   1659 atggaggaggctagggacatgtacccggttgtggtggcgcatcctgtacacagactaaat 1718

Qy   1519 cctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgca 1578
Db   1719 cctgctgacaggcggaggtcggtctcttcatcagccctcgatgccgacatccccagcgca 1778

Qy   1579 gatttttccttcagccagggatga 1602
Db   1779 gatttttccttcagccagggatga 1802
```

```
RESULT   9
AAF24585
ID   AAF24585 standard; DNA; 1886 BP.
XX
AC   AAF24585;
XX
DT   20-APR-2001  (first entry)
XX
DE   Nucleotide sequence of the wheat Mlo protein TrMlo3.
XX
KW   Wheat; fungal resistance; fungal pathogen; Erysiphe graminis; papillae;
KW   powdery mildew; Mlo; cell wall apposition; transgenic plant; ss.
XX
OS   Triticum sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             198..1802
FT                   /*tag= a
FT                   /product= "Mlo protein"
XX
PN   WO200078799-A2.
XX
PD   28-DEC-2000.
XX
PF   16-JUN-2000; 2000WO-EP05576.
XX
PR   18-JUN-1999;   99US-0336112.
XX
PA   (NOVS ) NOVARTIS AG.
PA   (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI   Salmeron JM,  Weislo LJ,  Strawn LJ,  Kramer CM,  Wang HX;
PI   Vernooij BT,  Levin JZ,  Heifetz PB,  Patton DA,  Que Q;
XX
DR   WPI; 2001-112311/12.
DR   P-PSDB; AAB31252.
XX
PT   Novel polynucleotide which encodes Mlo protein from wheat, useful for
PT   producing fungal resistant plants, in particular wheat plant  -
XX
PS   Claim 2; Page 97-99; 128pp; English.
XX
CC   The present sequence encodes a Mlo protein. Mlo proteins given
CC   resistance to fungal pathogens which infect living epidermal plant cells.
CC   Mlo proteins give proteins resistance to fungal pathogens, especially
CC   Erysiphe graminis (powdery mildews). In barley, mutations at the Mlo
CC   locus are responsible for a plant resistant pathotype. The mechanism
CC   of Mlo resistance involves the formation of large cell wall appositions,
CC   called papillae, at pathogen contact sites. Papillae mainly contain
CC   callose, but also carbohydrates, phenols and proteins. Polynucleotides
CC   encoding Mlo proteins are useful for making transgenic plants,
CC   preferably wheat, which are resistant to fungal pathogens.
XX
SQ   Sequence 1886 BP; 405 A; 564 C; 531 G; 386 T; 0 other;

  Query Match            81.5%;  Score 1305.6;  DB 22;  Length 1886;
  Best Local Similarity  89.9%;  Pred. No. 1.2e-268;
  Matches 1424;  Conservative    0;  Mismatches  154;  Indels    6;  Gaps    2;

Qy      22 ccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatg 81
           |||||||||  ||||||||||||||||||| ||||||||||| |||||||||||| ||||
Db     222 ccggcgcggacgctgccggagacgccgtcctgggcggtggcgctggtcttcgccgtcatg 281

Qy      82 gtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcac 141
             |  |||| |||||||| |||| ||||  |||||||||||||||||||||||||  |
Db     282 atcatcgtctccgtcctcctggagcacgcgctccacaagctcggccattggttccacaag 341

Qy     142 cggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtg 201
           |||||||||||  || |||  ||||||||||||||||||||||||||||||| |||||||||
Db     342 cggcacaagaacgcgctggcggaggcgctggagaagatgaaggcggagctgatgctggtg 401

Qy     202 ggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatc 261
           || ||||| || ||||| |||  ||||||||||||||    ||| ||  ||||||||||
Db     402 ggattcatctcgctgctgctcgccgtcacgcaggaccc---aatctccgggatatgcatc 458

Qy     262 tccgaggatgccgccgacgtcatgtggccctgcaagcgcggcaccgagggccgcaagccc 321
           ||| || | ||||||  | ||||| | |||||||||    |  |||    |  |||| |
Db     459 tcccagaaggccgccagcatcatgcgcccctgcaaggtggaacccggttccgtcaagagc 518

Qy     322 agcaagtacgttgactactgccc---ggagggcaaggtggcgctcatgtccacgggcagc 378
           |   | | |   |||||||| |    ||||||||||||||||||||||||||||||||
Db     519 aagtacaaggactactactgcgccaaagagggcaaggtggcgctcatgtccacgggcagc 578

Qy     379 ttgcaccagctgcacgtcttcatcttcgtgctcgcggtcttccatgtcacctacagcgtc 438
           ||||||||||| ||| | |||||||||||||| || ||||||||||||||||||||||||
Db     579 ctgcaccagctccacatattcatcttcgtgctagccgtcttccatgtcacctacagcgtc 638

Qy     439 atcaccatagctctaagccgtctcaaaatgagaacatggaagaaatgggagacagagacc 498
           |||| ||| |||||||||||||||||| ||||||||||||||||||||||||||||| |||
Db     639 atcatcatggctctaagccgtctcaagatgagaacatggaagaaatgggagacagaaacc 698

Qy     499 acctccttggaataccagttcgcaaatgatcctgcacggttccggttcacgcaccagacg 558
           |||||||||||||||||||||||||||||||||||| |||||||| ||||||||||||||
Db     699 gcctccttggaataccagttcgcaaatgatcctgcgcggttccgcttcacgcaccagacg 758

Qy     559 tcgttcgtgaagcgccacctgggcctctccagcacccctggcatcagatgggtggtggcc 618
           |||||||||||||| |||||||||||  |||||||||||  ||| ||||||||||||||||
Db     759 tcgttcgtgaagcggcacctgggcctgtccagcacccccggcgtcagatgggtggtggcc 818

Qy     619 ttcttcaggcagttcttcaggtcagtcaccaaggtggactacctgaccttgagggcaggc 678
           |||||||||||||||||||||||||| ||||||||||||||||||| ||||||||||||||
Db     819 ttcttcaggcagttcttcaggtcggtcaccaaggtggactacctcaccttgagggcaggc 878

Qy     679 ttcatcaacgcgcatttgtcgcaaaacagcaagttcgacttccacaagtacatcaagagg 738
           |||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||||
Db     879 ttcatcaacgcgcacttgtcgcagaacagcaagttcgacttccacaagtacatcaagagg 938

Qy     739 tcgatggaggacgacttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcg 798
           ||  |||||||||||||||||  |||||||| |||||||||||||||||||||||| |||||||
Db     939 tccatggaggacgacttcaaagtcgtcgttggcatcagcctcccgctgtgggctgtggcg 998

Qy     799 atcctcaccctcttccttgacatcaatggggttggcacgctcatctggatttctttcatc 858
           |||||||||||||||||||||| ||| | ||| | ||||| |||| |||| ||||||||||
Db     999 atcctcaccctcttccttgatatcgacgggatcggcacactcacctgggtttctttcatc 1058

Qy     859 cctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatggcc 918
           |||||| | ||||||||||||||||||||||||||||| ||||||||||||||| |||||||
Db    1059 cctctcatcatcctcttgtgtgttggaaccaagctagagatgatcatcatggggatggcc 1118

Qy     919 ctggagatccaggaccgggcgagcgtcatcaagggggcccccgtggtcgagcccagcaac 978
           |||||||||||||||||| |||||||||||||||||| ||||||||||||||||||||||
Db    1119 ctggagatccaggaccggtcgagcgtcatcaagggggcacccgtggtcgagcccagcaac 1178

Qy     979 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttgttc 1038
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db    1179 aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgctgttc 1238

Qy    1039 cagaacgcgtttcagatggcgcattttgtgtggacagtggccacgcccggcttgaagaaa 1098
           |||||||||||||||||||| ||||| |||||||||||||||||||||||||||||| |
Db    1239 cagaacgcgtttcagatggcacatttcgtgtggacagtggccacgcccggcttgaaggac 1298

Qy    1099 tgctaccacacgcagatcgggctgagcatcatgaaggtggtggtggggctagctctccag 1158
           |||| ||| | | | |||||||||||||||||||||||| ||| ||||||| ||||||||
Db    1299 tgcttccatatgaacatcgggctgagcatcatgaaggtcgtgctggggctggctctccag 1358

Qy    1159 ttcctctgcagctatatgaccttcccccctctacgcgctcgtcacacagatgggatcaaac 1218
           ||||| |||||||| || |||||||||||||||||||| ||||||||||||||||||||
Db    1359 ttcctgtgcagctacatcaccttcccccctctacgcgctagtcacacagatgggatcaaac 1418

Qy    1219 atgaagaggtccatcttcgacgagcagacgtccaaggcgctcaccaactggcggaacacg 1278
           |||||||||||||||||||||||||||||||  |||||||||| ||||||||||||||||
Db    1419 atgaagaggtccatcttcgacgagcagacagccaaggcgctgaccaactggcggaacacg 1478

Qy    1279 gccaaggagaagaagaaagtccgagacacggacatgctgatggctcagatgatcggcgac 1338
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Db    1479 gccaaggagaagaagaaggtccgagacacggacatgctgatggcgcagatgatcggcgac 1538

Qy    1339 gcaacaccgagccgaggctcgtcgccgatgccgagccgggggctcatcacccgtgcacctg 1398

Db    1539 gcaacacccagccgaggcacgtccccgatgcctagccgggggctcatcgccggtgcacctg 1598

Qy    1399 cttcacaagggcatgggcggtcggacgacccccagagcgcgcccacctcgccaaggacc 1458

Db    1599 cttcagaagggcatgggacggtctgacgatccccagagcgcaccgacctcgccaaggacc 1658

Qy    1459 cagcaggaggctagggacatgtacccggttgtggtggcgcacccggtgcacagactaaat 1518

Db    1659 atggaggaggctagggacatgtacccggttgtggtggcgcatcctgtacacagactaaat 1718

Qy    1519 cctaacgacaggaggaggtccgcctcgtcgtcggccctcgaagccgacatccccagtgca 1578

Db    1719 cctgctgacaggcggaggtcggtctcttcatcagccctcgatgccgacatccccagcgca 1778

Qy    1579 gatttttccttcagccagggatga 1602

Db    1779 gatttttccttcagccagggatga 1802
```

```
RESULT  10
AAV35030
ID   AAV35030 standard; cDNA; 1635 BP.
XX
AC   AAV35030;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO gene homologue.
XX
KW   Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS   Hordeum vulgare.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1635
FT                   /*tag=  a
FT                   /product= MLO protein homologue
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB02046.
XX
PR   07-MAR-1997;   97GB-0004789.
PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   P-PSDB; AAW59445.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Claim 9; Fig 11; 150pp; English.
XX
CC   The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC   exerts a negative regulatory function on a pathogen defence response,
CC   such that mutants exhibit a defence response in the absence of pathogen.
CC   Down-regulation or out-competition of Mlo function may be used to
CC   stimulate a defence response in transgenic plants conferring increased
CC   pathogen resistance, especially resistance to powdery mildew or rust.
CC   The product can also be used for identifying compounds able to
CC   stimulate a defence response in a plant by interaction with
CC   encoded polypeptide.
XX
SQ   Sequence 1635 BP; 315 A; 496 C; 520 G; 304 T; 0 other;
```

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  Query Match             58.5%;  Score 936.8;  DB 19;  Length 1635;
  Best Local Similarity   76.4%;  Pred. No. 3.8e-190;
  Matches 1270;  Conservative    0;  Mismatches  272;  Indels  120;  Gaps    5;

Qy      18 ggtgccggcgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgc 77

Db      12 ggcgggaggtcgggagctgtcggacacgccgacgtgggcggtggcggtagtctgcgccgt 71

Qy      78 catggtgctcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttcca 137

Db      72 catgatactcgtctccgtcgccatggagcacgcgctccacaagctcggccactggttcca 131

Qy     138 gcaccggcacaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgct 197

Db     132 caagtggcgcaagaaggccctgggggaggcgctggagaagatgaaggcggagctcatgct 191

Qy     198 ggtgggcttcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatg 257

Db     192 ggtgggcttcatatccctgctcctcatcgtcacgcaggatcc---cgtctccaggatctg 248

Qy     258 catctccgaggatgccgccgacgtcatgtggccctgcaagc------gcggcaccgaggg 311

Db     249 catctccaaggaggccggcgagaagatgctcccgtgcaagccttacgacggcgccggcgg 308

Qy     312 ccgcaagcccagcaagta---------------------------------------- 329

Db     309 tggcaaaggcaaggacaatcaccggaggcttctctggctccaaggcgagagcgagaccca 368

Qy     330 ------------------------------cgttgactactgcccggagggcaaggtggc 359

Db     369 ccgccggttcctggctgccccggccggagtggacgtctgcgccaaacagggcaaggtggc 428

Qy     360 gctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcgtgctcgcggtctt 419

Db     429 gctgatgtcagcgggaagcatgcaccaactgcacatattcatcttcgtgctcgccgtctt 488

Qy     420 ccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaatgagaacatggaa 479

Db     489 ccacgtcttgtacagcgtcgtcaccatgaccctaagccgtctcaaaatgaagcaatggaa 548

Qy     480 gaaatgggagacagagaccacctccttggaataccagttcgcaaatgatcctgcacggtt 539

Db     549 caagtgggagtcggagaccgcctcgctggagtatcagttcgcgaatgatccatcgcggtg 608

Qy     540 ccggttcacgcaccagacgtcgttcgtgaagcgccacctgggcctctccagcacccctgg 599

Db     609 ccggttcacgcaccagacgacgttggtgaggcggcacctgggcctctccagcaccccgg 668

Qy     600 catcagatgggtggtggccttcttcaggcagttcttcaggtcagtcaccaaggtggacta 659

Db     669 cgtcagatgggtggtggccttcttcaggcagttcttcacgtcggtgaccaaggtggacta 728

Qy     660 cctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaaacagcaagttcgactt 719

Db     729 cctgaccttgcggcagggcttcatcaacgcgcatctctcgcagggcaacaggttcgactt 788

Qy     720 ccacaagtacatcaagaggtcgatggaggacgacttcaaggtcgtcgtcggcatcagcct 779

Db     789 cgacaagtacatcaagaggtcgttggaggacgacttcaaagtcgtcgtccgcatcagtct 848

Qy     780 cccgctgtggggtgtggcgatcctcaccctcttccttgacatcaatggggttggcacgct 839

Db     849 caagctctggttcgtggcggtcctcatcctcttccttgatttcgacgggatcggcactct 908

Qy     840 catctggatttctttcatccctctcgtgatcctcttgtgtgttggaaccaagctggagat 899

Db     909 tctctggatgtccgtggttcctctcgtgatcctcttgtgggttgggaccaagctggagat 968
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```
Qy     900 gatcatcatggagatggccctggagatccaggaccgggcgagcgtcatcaaggggcccc 959
Db     969 ggtgatcatggagatggcccaggagatccatgaccgggagagcgtcgtcaagggtgctcc 1028

Qy     960 cgtggtcgagcccagcaacaagttcttctggttccaccgccccgactgggtcctcttctt 1019
Db    1029 cgccgtcgagcccagcaacaagtacttctggttcaaccggcctgactgggtcctcttcct 1088

Qy    1020 catacacctgacgttgttccagaacgcgtttcagatggcgcattttgtgtggacagtggc 1079
Db    1089 catgcacctcacactcttccagaacgcgtttcagatggctcatttcgtgtggacagtggc 1148

Qy    1080 cacgcccggcttgaagaaatgctaccacacgcagatcgggctgagcatcatgaaggtggt 1139
Db    1149 cacgcccggcttgaagaaatgctaccacgagaaaatggcaatgagcatcgccaaggtcgt 1208

Qy    1140 ggtggggctagctctccagttcctctgcagctatatgaccttccccctctacgcgctcgt 1199
Db    1209 gctgggggtagccgcccagatcttgtgcagctacatcaccttcccgctctacgcgctcgt 1268

Qy    1200 cacacagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgct 1259
Db    1269 cacgcagatgggctcacacatgaagagaagcatcttcgacgagcagacggccaaggcgct 1328

Qy    1260 caccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgat 1319
Db    1329 gaccaactggcgaaagatggccaaggagaagaagaaggcccgagacgcggccatgctgat 1388

Qy    1320 ggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccgggg 1379
Db    1389 ggcgcagatgggcggcggcgcgacgccgagcgtcggctcgtcgccg-------------- 1434

Qy    1380 ctcatcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgc 1439
Db    1435 ----------gtgcacctgctccacaaggccggggcgcggtccgacgacccccagagcgt 1484

Qy    1440 gcccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgca 1499
Db    1485 gccggcgtccccgagggccgagaaggaaggcggcggc--------------gtgcagca 1529

Qy    1500 cccggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcga 1559
Db    1530 tccggcgcgcaaggtacctccttgtgacgggtggaggtcggcctcgtcgccggcgctcga 1589

Qy    1560 agccgacatccccagtgcagatttttccttcagccagggatg 1601
Db    1590 cgctcacatccccggtgcagatttggcttcagcacgcaacg 1631
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RESULT  11
AAV35028
ID   AAV35028 standard; DNA; 1611 BP.
XX
AC   AAV35028;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Oryza sativa MLO gene homologue.
XX
KW   Rice; MLO; mildew; pathogen; resistance; ss.
XX
OS   Oryza sativa.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..1611
FT                   /*tag=  a
FT                   /product= MLO protein homologue
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;    97WO-GB02046.
XX
PR   07-MAR-1997;    97GB-0004789.
PR   29-JUL-1996;    96GB-0015879.
PR   30-OCT-1996;    96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
DR   P-PSDB; AAW59444.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Claim 6; Fig 10; 150pp; English.
XX
CC   The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC   exerts a negative regulatory function on a pathogen defence response,
CC   such that mutants exhibit a defence response in the absence of pathogen.
CC   Down-regulation or out-competition of Mlo function may be used to
CC   stimulate a defence response in transgenic plants conferring increased
CC   pathogen resistance, especially resistance to powdery mildew or rust.
CC   The product can also be used for identifying compounds able to
CC   stimulate a defence response in a plant by interaction with
CC   encoded polypeptide.
XX
SQ   Sequence 1611 BP; 348 A; 450 C; 450 G; 363 T; 0 other;
```

Query Match 47.8%; Score 765.6; DB 19; Length 1611;
Best Local Similarity 71.5%; Pred. No. 1.1e-153;
Matches 1151; Conservative 0; Mismatches 384; Indels 75; Gaps 8;

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Qy      26 cgcgggagctgccggagacgccgtcgtgggcggtggcggtggtcttcgccgccatggtgc 85
Db      23 cgcgggagttgccggagacgccgacgtgggcggtggccgtcgtctgcgccgtcctcgtgc 82

Qy      86 tcgtgtccgtcctcatggaacacggcctccacaagctcggccattggttccagcaccggc 145
Db      83 tcgtctccgccgccatggagcacggcctccacaacctcagcca-----taaaaccaccgc 137

Qy     146 acaagaaggccctgtgggaggcgctggagaagatgaaggcggagctcatgctggtgggct 205
Db     138 agaagttctcatatttcttgtcctatctgcactt----gcagagctgatgctgctgggct 193

Qy     206 tcatatccctgctcctcatcgtcacgcaggaccccatcatcgccaagatatgcatctccg 265
Db     194 tcatatccctgcttctcaccgtggcacaggcgcc---catctccaagatctgcatcccca 250

Qy     266 aggatgccgccgacgtcatgtggccctgcaag---------------------------- 297
Db     251 agtcggctgccaacatcttgttgccgtgcaaggcaggccaagatgccatcgaagaagaag 310

Qy     298 -----------cgcggcaccgagggccgcaagcccagcaagtacgttgactactgcccgg 346
Db     311 cagcaagtggtcgccggtccttggccggcgccggcggcggggactactgctcgaaattcg 370

Qy     347 agggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgtcttcatcttcg 406
Db     371 atggcaaggtggcgctgatgtcggcaaagagcatgcaccagctgcacattttcatcttcg 430

Qy     407 tgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaagccgtctcaaaa 466
Db     431 tgctcgccgtgttccatgttacctactgcatcatcaccatgggtttagggcgcctcaaaa 490

Qy     467 tgagaacatggaagaaatgggagacagagaccacctccttggaataccagttcgcaaatg 526
Db     491 tgaagaaatggaagaagtgggagtcacagaccaactcattggagtatcagttcgcaatcg 550

Qy     527 atcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcgccacctggg---cc 583
```

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Db    551 atccttcacgattcaggttcacgcatcagacgtcgttcgtgaagcggcatctgggatcat 610

Qy    584 tctccagcacccctggcatcagatgggtggtggccttcttcaggcagttcttcaggtcag 643
Db    611 tctcaagcacccctgggctcagatggatcgtagcattcttcaggcagttctttgggtccg 670

Qy    644 tcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgcatttgtcgcaaa 703
Db    671 tcaccaaggtggactacctgaccatgcggcaaggcttcatcaatgcgcatttgtcgcaga 730

Qy    704 acagcaagttcgacttccacaagtacatcaagaggtcgatggaggacgacttcaaggtcg 763
Db    731 atagcaagttcgacttccacaaatacatcaagaggtctttggaggacgacttcaaagttg 790

Qy    764 tcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctcttccttgacatca 823
Db    791 tcgttggcatcagcctccctctgtggttcgtcggaatccttgtactcttcctcgatatcc 850

Qy    824 atggggttggcacgctcatctggatttctttcatccctctcgtgatcctcttgtgtgttg 883
Db    851 acggtcttggcacacttatttggatctcttttgttcctctcatcatcgtcttgttagttg 910

Qy    884 gaaccaagctggagatgatcatcatggagatggccctggagatccaggaccgggcgagcg 943
Db    911 ggaccaagctagagatggtgatcatggagatggcccaagagatacaggacagggccactg 970

Qy    944 tcatcaaggggcccccgtggtcgagcccagcaacaagttcttctggttccaccgccccg 1003
Db    971 tgatccagggagcacctatggttgaaccaagcaacaagtacttctggttcaaccgccctg 1030

Qy   1004 actgggtcctcttcttcatacacctgacgttgttccagaacgcgtttcagatggcgcatt 1063
Db   1031 actgggtcttgtttttcatacacctgacactcttccataacgcatttcagatggcgcatt 1090

Qy   1064 ttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgcagatcgggctga 1123
Db   1091 tcgtatggactatggcaacacctggtctgaagaaatgcttccatgaaaatatttggctga 1150

Qy   1124 gcatcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgaccttcc 1183
Db   1151 gcatcgtggaagtcattgtggggatctctcttcaggtgctatgcagctacatcaccttcc 1210

Qy   1184 ccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacgagc 1243
Db   1211 cgctctacgcgctcgtcacacagatgggatcgaacatgaagaagacaattttcgaggagc 1270

Qy   1244 agacgtccaaggcgctcaccaactggcggaacacggccaaggagaagaagaaagtccgag 1303
Db   1271 aaacgatgaaggcgctgatgaactggaggaagaaggcgatggagaagaagaaggtccggg 1330

Qy   1304 acacggacatgctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtcgc 1363
Db   1331 acgccgacgcgttcctggcgcagatgagcgtcgac----------------ttcgcgacgc 1375

Qy   1364 cgatgccgagccggggctcatcacccgtgcacctgcttcacaagggcatggggcggtcgg 1423
Db   1376 cggcgtcgagccggtccgcgtcgccggtgcacctgctgc---aggtcacagggcgggtcg 1432

Qy   1424 acgacccccagagcgcgcccacctcgccaaggacccagcaggaggctagggacatgtacc 1483
Db   1433 gacgcccgccgagcccaatcacggtggcctcaccaccggcaccggaggaggacatgtacc 1492

Qy   1484 cggttgtggtggcgcacccggtgcacagactaaatcctaacgacaggaggaggtccgcct 1543
Db   1493 cggtgccggcggcggctgcgtctccgccagct---gctagacgacccgccggacaggaggt 1549

Qy   1544 cgtcgtcggccctcgaagccgacatccccagtgcagatttttccttcagc 1593
Db   1550 ggatggcatcctcgtcggccgacatcgccgattctgatttttccttcagc 1599

RESULT 12
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AAV35025
ID   AAV35025 standard; DNA; 2425 BP.
XX
AC   AAV35025;
XX
DT   13-OCT-1998  (first entry)
XX
DE   Hordeum vulgare MLO gene homologue.
XX
KW   Barley; MLO; mildew; pathogen; resistance; ss.
XX
OS   Hordeum vulgare.
XX
PN   WO9804586-A2.
XX
PD   05-FEB-1998.
XX
PF   29-JUL-1997;   97WO-GB02046.
XX
PR   07-MAR-1997;   97GB-0004789.
PR   29-JUL-1996;   96GB-0015879.
PR   30-OCT-1996;   96GB-0022626.
XX
PA   (INNE-) INNES CENT INNOVATIONS LTD JOHN.
XX
PI   Bueschges R,  Panstruga R,  Schulzelefert PMJ;
XX
DR   WPI; 1998-159149/14.
XX
PT   New isolated Mlo gene of barley - used to develop products for the
PT   production of transgenic plants which have increased pathogen
PT   resistance
XX
PS   Disclosure; Fig 6; 150pp; English.
XX
CC   The sequence is that of a homologue of the MLO gene, wild-type Mlo
CC   exerts a negative regulatory function on a pathogen defence response,
CC   such that mutants exhibit a defence response in the absence of pathogen.
CC   Down-regulation or out-competition of Mlo function may be used to
CC   stimulate a defence response in transgenic plants conferring increased
CC   pathogen resistance, especially resistance to powdery mildew or rust.
CC   The product can also be used for identifying compounds able to
CC   stimulate a defence response in a plant by interaction with
CC   encoded polypeptide.
XX
SQ   Sequence 2425 BP; 525 A; 692 C; 596 G; 612 T; 0 other;
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  Query Match             35.8%;  Score 573;  DB 19;  Length 2425;
  Best Local Similarity   84.1%;  Pred. No. 1.2e-112;
  Matches  741;  Conservative    0;  Mismatches    5;  Indels  135;  Gaps    3;

Qy     857 tccctctcgtgatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatgg 916
Db    1529 ttcctcaacagatcctcttgtgtgttggaaccaagctggagatgatcatcatggagatgg 1588

Qy     917 ccctggagatccaggaccgggcgagcgtcatcaagggggcccccgtggtcgagcccagca 976
Db    1589 ccctggagatccaggaccgggcgagcgtcatcaagggggcccccgtggtcgagcccagca 1648

Qy     977 ac-aagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttg 1035
Db    1649 acaaagttcttctggttccaccgccccgactgggtcctcttcttcatacacctgacgttg 1708

Qy    1036 ttccagaacgcgtttcagatggcgcattttgtgtggacagt------------------- 1076
Db    1709 ttccagaacgcgtttcagatggcgcattttgtgtggacagtggtacgccaccgatgaact 1768

Qy    1077 ---------------------------------------------------------- 1076

Db    1769 tgtcagttaacatgggtgtcaaggcaccgagtgccgctgatgaactgctctgacggagat 1828

Qy    1077 ----------ggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagc 1125
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Db    1829 ttactgttgtaggccacgcccggcttgaagaaatgctaccacacgcagatcgggctgagc 1888

Qy    1126 atcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgaccttcccc 1185
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1889 atcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgaccttcccc 1948

Qy    1186 ctctacgcgctcgtcaca---------------------------------------- 1203
           ||||||||||||||||||
Db    1949 ctctacgcgctcgtcacacaggtaataaaaccgtaatcatctgtgtgtgctggctttgta 2008

Qy    1204 --cagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctca 1261
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2009 tgcagatgggatcaaacatgaagaggtccatcttcgacgagcagacgtccaaggcgctca 2068

Qy    1262 ccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatgg 1321
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2069 ccaactggcggaacacggccaaggagaagaagaaagtccgagacacggacatgctgatgg 2128

Qy    1322 ctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggct 1381
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2129 ctcagatgatcggcgacgcaacaccgagccgaggctcgtcgccgatgccgagccggggct 2188

Qy    1382 catcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgc 1441
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2189 catcacccgtgcacctgcttcacaagggcatggggcggtcggacgacccccagagcgcgc 2248

Qy    1442 ccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcacc 1501
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2249 ccacctcgccaaggacccagcaggaggctagggacatgtacccggttgtggtggcgcacc 2308

Qy    1502 cggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaag 1561
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2309 cggtgcacagactaaatcctaacgacaggaggaggtccgcctcgtcgtcggccctcgaag 2368

Qy    1562 ccgacatccccagtgcagatttttccttcagccagggatga 1602
           ||||||||||||||||||||||||||||||||||||||||
Db    2369 ccgacatccccagtgcagatttttccttcagccagggatga 2409


RESULT  13
AAA52707
ID   AAA52707 standard; cDNA; 678 BP.
XX
AC   AAA52707;
XX
DT   27-OCT-2000  (first entry)
XX
DE   Wheat Mlo homologue putative coding sequence #1.
XX
KW   Wheat; Mlo homologue; disease resistance; ss.
XX
OS   Triticum aestivum.
XX
FH   Key             Location/Qualifiers
FT   CDS             3..664
FT                   /*tag= a
FT                   /product= "Mlo homologue"
FT                   /partial
FT                   /transl_except= (pos:639..640,aa:Ser)
FT                   /note= "there is an apparent one nucleotide
FT                   deletion at this position, resulting in a frameshift"
XX
PN   WO200036110-A2.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US30181.
XX
PR   18-DEC-1998;   98US-0112737.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE,  Miao G,  Rafalski JA,  Fang Y,  Sakai H,  Taramino G;
XX
DR   WPI; 2000-431590/37.
DR   P-PSDB; AAB01797.
XX
PT   New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT   creating transgenic plants with altered levels of disease resistance -
XX
PS   Claim 2; Page 52; 79pp; English.
XX
CC   The present sequence is a putative coding sequence for a Mlo homologue
CC   from wheat. It was identified by searching a root and leaf cDNA library
CC   for sequences encoding proteins similar to Mlo from Hordeum vulgare
CC   (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
CC   graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC   priming of disease resistance even if the pathogen is not present. The
CC   gene and protein can be used to create transgenic plants which have
CC   increased disease resistance, as well as allowing researchers to find
CC   other resistance-conferring genes and proteins.
XX
SQ   Sequence 678 BP; 143 A; 206 C; 199 G; 130 T; 0 other;


  Query Match             35.6%;  Score 569.8;  DB 21;  Length 678;
  Best Local Similarity   92.0%;  Pred. No. 4.3e-112;
  Matches  612;  Conservative    0;  Mismatches   52;  Indels    1;  Gaps    1;

Qy     938 cgagcgtcatcaaggggcccccgtggtcgagcccagcaacaagttcttctggttccacc 997
           |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||
Db       4 cgagcgtcatcaaggggcgcccgtggttgagcccagcaacaagttcttctggttccacc 63

Qy     998 gccccgactgggtcctcttcttcatacacctgacgttgttccagaacgcgtttcagatgg 1057
           |||||||||||||||||||||||||||||||||||| |||||||||| ||||||||||||
Db      64 gccccgactgggtcctcttcttcatacacctgacgctgttccagaatgcgtttcagatgg 123

Qy    1058 cgcattttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgcagatcg 1117
           | ||||| || ||||||||||||||||||||||||||||||||| ||| | ||| ||||
Db     124 cacatttcgtctggacagtggccacgcccggcttgaagaaatgcttccatatgcacatcg 183

Qy    1118 ggctgagcatcatgaaggtggtggtggggctagctctccagttcctctgcagctatatga 1177
           | |||||||||||||||| ||| ||||||| ||||| ||||||||||||||||||| |
Db     184 gtctgagcatcatgaaggtcgtgctggggctggctcttcagttcctctgcagctatatca 243

Qy    1178 ccttccccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccatcttcg 1237
           |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db     244 ccttccccctctacgcgctcgtcacacagatgggatcgaacatgaagaggtccatcttcg 303

Qy    1238 acgagcagacgtccaaggcgctcaccaactggcggaacacggccaaggagaagaagaaag 1297
           |||||||||||| |||||||||| ||||||||||||||||||||||||||||||||| |
Db     304 acgagcagacggccaaggcgctgaccaactggcggaacacggccaaggagaagaagaagg 363

Qy    1298 tccgagacacggacatgctgatggctcagatgatcggcgacgcaacaccgagccgaggct 1357
           |||||||||||||||||||||||| |||||||||||||||| || || |||||||||
Db     364 tccgagacacggacatgctgatggcgcagatgatcggcgacgcgacgcccagccgaggca 423

Qy    1358 cgtcgccgatgccgagccggggctcatcacccgtgcacctgcttcacaagggcatggggc 1417
           |||||||||||||| |||||||  || ||||| ||||||||||||||||||||||||| |
Db     424 cgtcgccgatgcctagccgggcttcgtcaccggtgcacctgcttcacaagggcatgggac 483

Qy    1418 ggtcggacgacccccagagcgcgccgacctcgccaaggacccagcaggaggctagggaca 1477
           |||| ||||| |||||||||||||| ||||||||||||||  | ||||||||||||||||
Db     484 ggtccgacgatccccagagcgcgccgacctcgccaaggaccatggaggaggctagggaca 543

Qy    1478 tgtacccggttgtggtggcgcacccggtgcacagactaaatcctaacgacaggaggaggt 1537
           |||||||||||||||||||| || ||||||||||||||||   |||||| ||||||
Db     544 tgtacccggttgtggtggcgcatcccgtgcacagactaaatcctgctgacaggcggaggt 603

Qy    1538 ccgcctcgtcgtcggccctcgaagccgacatccccagtgcagatttttccttcagccagg 1597
           | | ||| ||||||| ||||| |||||||| ||||| ||||||||||||||| |||||
Db     604 cggtctcttcgtcgggactcgaggccgacat-cccagcgcagatttttccttcaaccagg 662

Qy    1598 gatga 1602
           |||||
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Db    663 gatga 667


RESULT  14
AAA52704
ID   AAA52704 standard; cDNA; 563 BP.
XX
AC   AAA52704;
XX
DT   27-OCT-2000  (first entry)
XX
DE   Soybean Mlo homologue putative coding sequence #2.
XX
KW   Soybean; Mlo homologue; disease resistance; ss.
XX
OS   Glycine max.
XX
FH   Key             Location/Qualifiers
FT   CDS             2..562
FT                   /*tag= a
FT                   /product= "Mlo homologue"
FT                   /partial
FT                   /transl_except= (pos:452..455,aa:Xaa)
FT                   /transl_except= (pos:503..505,aa:Xaa)
FT                   /transl_except= (pos:530..532,aa:Xaa)
FT                   /transl_except= (pos:557..559,aa:Xaa)
FT                   /note= "Xaa=unknown"
XX
PN   WO200036110-A2.
XX
PD   22-JUN-2000.
XX
PF   17-DEC-1999;   99WO-US30181.
XX
PR   18-DEC-1998;   98US-0112737.
XX
PA   (DUPO ) DU PONT DE NEMOURS & CO E I.
XX
PI   Cahoon RE,  Miao G,  Rafalski JA,  Fang Y,  Sakai H,  Taramino G;
XX
DR   WPI; 2000-431590/37.
DR   P-PSDB; AAB01794.
XX
PT   New polynucleotide encoding a Mlo homologue polypeptide, useful for
PT   creating transgenic plants with altered levels of disease resistance -
XX
PS   Claim 2; Page 47; 79pp; English.
XX
CC   The present sequence is a putative coding sequence for a Mlo homologue
CC   from the soybean. It was identified by searching a seed cDNA library
CC   for sequences encoding proteins similar to Mlo from Hordeum vulgare
CC   (barley) and Arabidopsis thaliana. Mlo confers resistance to Erysiphe
CC   graminis f. sp. hordei upon the plant, and its inactivation leads to the
CC   priming of disease resistance even if the pathogen is not present. The
CC   gene and protein can be used to create transgenic plants which have
CC   increased disease resistance, as well as allowing researchers to find
CC   other resistance-conferring genes and proteins.
XX
SQ   Sequence 563 BP; 118 A; 171 C; 165 G; 105 T; 4 other;


  Query Match             30.8%;  Score 493.4;  DB 21;  Length 563;
  Best Local Similarity   92.0%;  Pred. No. 7.5e-96;
  Matches  518;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy    942 cgtcatcaaggggcccccgtggtcgagcccagcaacaagttcttctggttccaccgccc 1001
          ||||||||||||||| |||||||| ||||||||||||||||||||||||||||||||||
Db      1 cgtcatcaaggggcgcccgtggttgagcccagcaacaagttcttctggttccaccgccc 60

Qy   1002 cgactgggtcctcttcttcatacacctgacgttgttccagaacgcgtttcagatggcgca 1061
          |||||||||||||||||||||||||||||| |||||||||| |||||||||||||| ||
Db     61 cgactgggtcctcttcttcatacacctgacgctgttccagaatgcgtttcagatggcaca 120

Qy   1062 ttttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgcagatcgggct 1121
          ||| || |||||||||||||||||||||||||||||||||| ||| | ||| ||||| ||
Db    121 tttcgtctggacagtggccacgcccggcttgaagaaatgcttccatatgcacatcggtct 180

Qy   1122 gagcatcatgaaggtggtggtggggctagctctccagttcctctgcagctatatgacctt 1181
          |||||||||||||||| ||| ||||||| ||||| ||||||||||||||||||||| |||||
Db    181 gagcatcatgaaggtcgtgctggggctggctcttcagttcctctgcagctatatcacctt 240

Qy   1182 ccccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccatcttcgacga 1241
          |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db    241 ccccctctacgcgctcgtcacacagatgggatcgaacatgaagaggtccatcttcgacga 300

Qy   1242 gcagacgtccaaggcgctcaccaactggcggaacacggccaaggagaagaagaaagtccg 1301
          ||||||| |||||||||| ||||||||||||||||||||||||||||||||||||| |||||
Db    301 gcagacggccaaggcgctgaccaactggcggaacacggccaaggagaagaagaaggtccg 360

Qy   1302 agacacggacatgctgatggctcagatgatcggcgacgcaacaccgagccgaggctcgtc 1361
          |||||||||||||||||||| |||||||||||||||| || || ||||||||| ||||
Db    361 agacacggacatgctgatggcgcagatgatcggcgacgcgacgcccagccgaggcacgtc 420

Qy   1362 gccgatgccgagccggggctcatcacccgtgcacctgcttcacaagggcatggggcggtc 1421
          ||||||||| |||||||  || ||||| ||||| ||||||||||||||||||||| |||||
Db    421 gccgatgcctagccgggcttcgtcaccggtgcanctgcttcacaagggcatgggacggtc 480

Qy   1422 ggacgacccccagagcgcgcccacctcgccaaggacccagcaggaggctagggacatgta 1481
          |||||  |||||||||||||| | |||||||||||||  | |||| |||| |||||||||
Db    481 cgacgattcccagagcgcgccganctcgccaaggaccatggaggaagctanggacatgta 540

Qy   1482 cccggttgtggtggcgcacccgg 1504
          ||||||||||||||||| || |
Db    541 cccggttgtggtggcgcancccg 563


RESULT  15
AAZ49564
ID   AAZ49564 standard; cDNA; 1815 BP.
XX
AC   AAZ49564;
XX
DT   07-APR-2000  (first entry)
XX
DE   Maize MLO6 protein encoding cDNA.
XX
KW   MLO6 protein; ZmMLO6; chromosome 5; mutation; recessive allele;
KW   disease resistance; pathogen; anti-infective; antipathogenic; antiviral;
KW   antifungal; antihelminthic; anti-arthropod; maize; ss.
XX
OS   Zea mays.
XX
FH   Key             Location/Qualifiers
FT   CDS             46..1593
FT                   /*tag= a
FT                   /product= "MLO6 protein"
XX
PN   WO200001722-A1.
XX
PD   13-JAN-2000.
XX
PF   07-JUL-1999;   99WO-US15255.
XX
PR   07-JUL-1998;   98US-0091875.
XX
PA   (PION-) PIONEER HI-BRED INT INC.
XX
PI   Briggs SP,  Simmons CR;
XX
DR   WPI; 2000-137196/12.
DR   P-PSDB; AAY44605.
XX
PT   Creating or enhancing disease resistance in plants by modulating plant
PT   resistance genes expression  -
XX
PS   Claim 1c; Page 70-71; 88pp; English.
```

XX
CC The present cDNA sequence (ATCC 98727) encodes maize MLO6 (ZmMLO6)
CC protein. Mlo6 gene is mapped to chromosome 5. It is a mutation-induced
CC recessive allele, that confers resistance to plant pathogens. Expression
CC of native Mlo genes in plants can be altered by transforming them with a
CC DNA construct comprising the mutated Mlo gene. Decreasing the expression
CC or activity of native MLO protein leads to enhanced resistance of plants
CC against pathogens such as fungi, virus, nematodes and insects. Mlo gene
CC can be used to isolate related sequences from other plants and as
CC molecular markers used in breeding programs aimed at improving disease
CC resistance. MLO protein has anti-infective, antipathogenic, antiviral,
CC antifungal, antihelminthic and anti-arthropod activity.
XX
SQ Sequence 1815 BP; 394 A; 551 C; 502 G; 368 T; 0 other;

Query Match 26.5%; Score 425.2; DB 21; Length 1815;
Best Local Similarity 66.0%; Pred. No. 3.2e-81;
Matches 632; Conservative 0; Mismatches 323; Indels 3; Gaps 1;

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Qy    336 ctactgcccggagggcaaggtggcgctcatgtccacgggcagcttgcaccagctgcacgt 395
          | | ||||| ||||| || ||| ||||||| ||||    |  | ||||||||||||||| |
Db    552 caagtgccccgaggggaaagtgccgctcatctccatcaacgccctgcaccagctgcacat 611

Qy    396 cttcatcttcgtgctcgcggtcttccatgtcacctacagcgtcatcaccatagctctaag 455
          |||||||||| | ||||| |||||||| ||| ||||||||  |||||||| || ||  |
Db    612 cttcatcttcttcctcgccgtcttccacgtctcctacagcgcaatcaccatggcgctcgg 671

Qy    456 ccgtctcaaaatgagaacatggaagaaatgggagacagagaccacctccttggaatacca 515
          | |   ||| ||  |  |||||||  | ||||||| ||| | |       || ||| |
Db    672 cagggccaagatacgtgcatggaaagagtgggagaaagaagctgcaggacaagactacga 731

Qy    516 gttcgcaaatgatcctgcacggttccggttcacgcaccagacgtcgttcgtgaagcgcca 575
          |||| || |||| ||  | |||||| ||||||| ||| |||| || ||||||| ||  ||
Db    732 gttctcacatgacccgacgcggttcaggttcacccacgagacttccttcgtgaggcagca 791

Qy    576 cctg---ggcctctccagcacccctggcatcagatgggtggtggcctttcttcaggcagtt 632
            ||   |  ||  ||   ||| |       |   |     ||||||| |||||||
Db    792 tatgaatgtgctgaacaagttcccagcatcattctacatcagcaacttcttccggcagtt 851

Qy    633 cttcaggtcagtcaccaaggtggactacctgaccttgagggcaggcttcatcaacgcgca 692
          ||||||||| || |  |||  ||||||    |  || |     ||||  ||||||  ||
Db    852 cttcaggtccgtgaggcaggcagactactgcgcgctgcgccacagctttgtcaacgtcca 911

Qy    693 tttgtcgcaaaacagcaagttcgacttccacaagtacatcaagaggtcgatggaggacga 752
          | || | |    |||||||||| || ||||| |||||||||||| ||||  ||||||| ||
Db    912 tctggcccctggcagcaagtttgatttccagaagtacatcaagcggtctctggaggatga 971

Qy    753 cttcaaggtcgtcgtcggcatcagcctcccgctgtggggtgtggcgatcctcaccctctt 812
          |||||||||  |||| || ||||| |  || |||||||| |   ||  || ||  ||||||
Db    972 cttcaaggtgatcgtggggatcagtcctcctctgtgggcttctgctctcatcttcctctt 1031

Qy    813 ccttgacatcaatggggttggcacgctcatctggatttctttcatccctctcgtgatcct 872
          |||  || |||||||      |||  |  |||||||  ||  |||| ||  | ||||||  |
Db   1032 cctcaacgtcaatggatggcacaccatgctctggatctccatcatgccggtggtgatcat 1091

Qy    873 cttgtgtgttggaaccaagctggagatgatcatcatggagatggccctggagatccagga 932
          | |||  || || || |||||| ||   ||||||      |||||  | || |||  |||
Db   1092 cctgtcggtggggacgaagctgcagggcatcatctgccgcatggcgatcgacatcacgga 1151

Qy    933 ccgggcgagcgtcatcaaggggggccccccgtggtcgagcccagcaacaagttcttctggtt 992
            ||       ||||||| ||||   |||  ||||  |   |||| ||   | |||||||||
Db   1152 gcgccacgccgtcatccagggcatcccgatggtgcaagtcagcgactcctacttctggtt 1211

Qy    993 ccaccgccccgactgggtcctcttcttcatacacctgacgttgttccagaacgcgtttca 1052
          |   ||||||  ||  || |||||| |||| ||| | ||  | |||||||| |  || ||
Db   1212 cgcacgccccaccttcgtgctcttcctcatccacttcaccctcttccagaatggcttcca 1271

Qy   1053 gatggcgcattttgtgtggacagtggccacgcccggcttgaagaaatgctaccacacgca 1112
          |||     | ||  | ||||   ||      |  |||| || |    |||| | ||
Db   1272 gatcatctacttcctctggattctgtatgagtacggcatggactcgtgcttcaacgactc 1331

Qy   1113 gatcgggctgagcatcatgaaggtggtggtggggctagctctccagttcctctgcagcta 1172
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                | | |   | |        |     | ||  | | | ||||| | || ||||||||
Db   1332 cgaagagttcgtctttgcacgactctgccttggcgtggttgtccaggtgctgtgcagcta 1391

Qy   1173 tatgaccttccccctctacgcgctcgtcacacagatgggatcaaacatgaagaggtccat 1232
            ||||  |||| || |||||||||||| | || ||||| || | |||||||  ||||||
Db   1392 cgtgacgctcccgctgtacgcgctcgtctcccaaatgggctccaccatgaagcagtccat 1451

Qy   1233 cttcgacgagcagacgtccaaggcgctcaccaactggcggaacacggccaaggagaag 1290
          |||||||||||||||| ||||||||||||  ||||||||   |   |||||| |||||
Db   1452 cttcgacgagcagacctccaaggcgctcaagaactggcgcgccggcgccaagaagaag 1509
```

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Job time: 5208 sec